

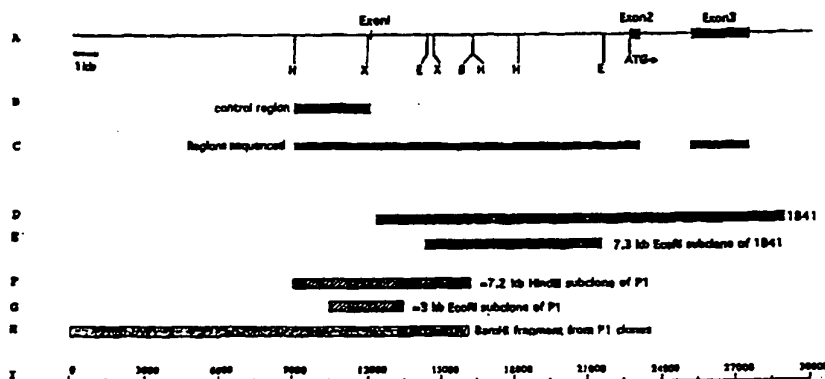
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(54) Title: MODULATORS OF ob GENE AND SCREENING METHODS THEREFOR



(57) Abstract

This invention relates to the isolation and cloning of the promoter and other control regions of a human *ob* gene. It provides a method for identifying and screening for agents useful for the treatment of diseases and pathological conditions affected by the level of expression of an *ob* gene. These agents interact directly or indirectly with the promoter or other control regions of the *ob* gene. A PPAR- γ agonist, BRL49653, has been identified to be useful in treating anorexia, cachexia, and other diseases characterized by insufficient food intake or body weight loss. Modulators of *ob* gene expression may be used to treat other diseases such as obesity, diabetes, hypertension, cardiovascular diseases and infertility.

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MODULATORS OF ob GENE AND SCREENING METHODS THEREFORCross Reference to Related Applications

This application is a continuation-in-part
5 application of a U.S. Application Serial No. 08/558,588
entitled "Modulators of ob Gene and Screening Methods
Therefor," filed October 30, 1995, by Briggs et al., which is
a continuation-in-part of U.S. Application Serial No.
08/510,584, entitled "Modulators of ob Gene and Screening
10 Methods Therefor," filed August 2, 1995, by Briggs et al.,
which is a continuation-in-part of U.S. Application Serial No.
08/418,096, entitled "Modulators of ob Gene and Screening
Methods Therefor," filed April 5, 1995, by Briggs et al.,
which is a continuation-in-part of U.S. Application Serial No.
15 08/408,584, entitled "Modulators of ob Gene and Screening
Methods Therefor," filed March 20, 1995, by Briggs et al., the
disclosure of which are incorporated by reference herein,
including drawings, tables and sequence listings.

Other priority applications include provisional
20 applications entitled "Modulators of ob Gene and Screening
Methods Therefor," filed by Briggs et al. on December 14, 1995
(Serial No. 60/008,601), November 30, 1995 (Serial No.
60/007,721), and November 21, 1995 (Serial No. 60/007,390),
the disclosure of which are incorporated by reference herein,
25 including drawings, tables and sequence listings.

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FIELD OF THE INVENTION

This invention relates to a method for screening for agents useful for treatment of diseases and pathological conditions affected by *ob* genes, and agents and compositions identified using such screening method. This invention also relates to regulatory elements and promoter sequences which serve to promote transcription of the *ob* gene.

BACKGROUND OF THE INVENTION

Obesity is usually defined as a body weight more than 20% in excess of the ideal body weight. Obesity is associated with an increased risk for cardiovascular disease, diabetes and an increased mortality rate (see Grundy et al., Disease-a-Month 36:645-696, 1990). Treatment for obesity includes diet, exercise and surgery (Leibel, R.L. et al., New England Journal of Medicine 332:621-628, 1995).

At least five single-gene mutations resulting in obesity have been described in mice, implicating genetic factors in the etiology of obesity (Friedman et al., Cell 69:217-220, 1990). In the *ob* mouse, a single gene mutation, obese, results in profound obesity, which is accompanied by diabetes (Friedman et al., Genomics 11:1054-1062, 1991). Cross-circulation experiments have suggested that *ob* mice are deficient of a blood-borne factor regulating nutrient intake and energy metabolism (Coleman, D.L., Diabetologia 14:141-148, 1978).

Zhang et al., Nature 372:425-432, 1994, not admitted to be prior art, describe cloning and sequencing the mouse *ob* gene and its human homologue. They indicate that the *ob* gene is exclusively expressed in white adipose tissue.

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SUMMARY OF THE INVENTION

Loss of appetite, diminished food intake, and loss of body weight are problems associated with many diseases. In the scope of the present invention it has been found that a down regulator of *ob* gene expression, BRL49653, i.e. 5-[[4-[2-(methyl-2-pyridinylamino)ethoxy]phenyl]methyl]-2,4-thiazolidinedione, has the properties of increasing food intake and body weight in rats. The administration of an effective amount of an *ob* gene down regulator will be able to treat a patient suffering from anorexia, cachexia and other wasting diseases characterized by loss of appetite, diminished food intake or body weight loss.

Also in the scope of the present invention, it has been found that up regulators of *ob* gene expression, glucocorticoids, have the properties of decreasing food consumption and body weight gain in rats. The administration of an effective amount of an *ob* gene up regulator will be able to treat a patient suffering from excessive food consumption and obesity, and related pathological conditions such as type II adult onset diabetes, infertility (Chehab, et al. Nature Genetics, 12:318-320, 1996, not admitted to be prior art), hypercholesterolemia, hyperlipidemia, cardiovascular diseases and hypertension.

By "*ob* gene" is meant a gene encoding a contiguous amino acid sequence sharing about at least 60% (preferably 75%, and more preferably 95%) identity with the human *ob* gene amino acid sequence disclosed on page 430 of Zhang et al., Nature 372:425-432, 1994, including, but not limited to, the human *ob* gene and the mouse *ob* gene disclosed in Zhang et al. id.

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Without being bound by any theory, Applicant proposes that the effects of BRL49653 and glucocorticoids on food intake and body weight mass are mediated through the level of *ob* gene expression. Therefore, body weight
5 homeostasis may be modulated by compounds regulating the expression of *ob* gene. Some of these compounds are disclosed in this application. Others will be identified by the methods disclosed in this application.

Accordingly, the present invention is also related
10 to the isolation, cloning and identification of the promoter and other regulatory elements of the *ob* gene and the use of *ob* gene control regions to screen for agents that modulate *ob* gene expression and thence use these modulators as lead
15 compounds to design or search for other drugs to treat disease related to the level of *ob* gene expression. The isolated *ob* gene control regions have utility in constructing in vitro and in vivo experimental models for studying the modulation of *ob* gene expression and assaying for modulators of *ob* gene
20 expression. Such experimental models make it possible to screen large collections of natural, semisynthetic, or synthetic compounds for therapeutic agents that affect *ob* gene expression.

The *ob* gene modulators identified by the methods of this invention may be used to control a variety of
25 physiological or biochemical conditions in animals (esp. mammals) such as the level of metabolism, body weight, food intake, oxygen consumption, body temperature, serum insulin level, serum glucose level, body fat content (versus muscle content) and the level of physical activities. Such
30 modulators are useful in treating a host with abnormal levels

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of *ob* gene expression, as well as those having normal levels of *ob* gene expression. The *ob* gene modulators may also be used to treat diseases and conditions affected by the level of *ob* gene expression, such as, but not limited to, obesity, hypercholesterolemia, hyperlipidemia, cardiovascular diseases, hypertension, diabetes, infertility, anorexia, cachexia and other wasting diseases characterized by loss of appetite, diminished food intake or body weight loss. The modulators are useful in mimicking human diseases or conditions in animals relating to the level of *ob* gene expression, such as, obesity, hypercholesterolemia, hyperlipidemia, cardiovascular diseases, hypertension, diabetes, infertility, anorexia, cachexia and other wasting diseases characterized by loss of appetite, diminished food intake or body weight loss. Such modulators of *ob* gene expression may be used to increase circulating levels of *ob* protein (i.e. leptin), the physiological consequences of which include the normalization of insulin and glucose levels (Pelleymounter, M.A. et al. Science 269:540-543, 1995; Halaas, J.L. et al. Science 269:543-546, 1995; Campfield, L.A. et al. Science 269:546-549, 1995; not admitted to be prior art). The modulators may be used in experimental testing of *ob* gene modulators for veterinary uses, including, but not limited to, controlling the body weight of animals and the fat content of meat.

Thus, in one aspect, the present invention is directed to an isolated, purified, enriched or recombinant nucleic acid containing a control region of a mammalian *ob* gene from, including, but not limited to, human, rat, mouse, pig, cattle, dog, or cat. In a preferred embodiment, the control region is from the human *ob* gene.

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By "control region" is meant a nucleic acid sequence capable of, required for, assisting or impeding initiating, terminating, or otherwise regulating the transcription of a gene, including, but not limited to, promoter, enhancer, 5 silencer and other regulatory elements (e.g. those regulating pausing or anti-termination). A positive transcription element increases the transcription of the ob gene. A negative transcription element decreases the transcription of the ob gene. The term "control region" does not include the 10 initiation or termination codons and other sequences already described in Zhang et al., supra. A control region also includes a nucleic acid sequence that may or may not be sufficient by itself to initiate, terminate, or otherwise regulate the transcription, yet is able to do so in 15 combination or coordination with other nucleic acid sequences. A control region can be in nontranscribed regions of a gene, introns or exons. A control region can be in the 5' upstream region or the 3' downstream region to the amino acid coding sequence. A control sequence can be a single regulatory 20 element from a gene. A control region can also have several regulatory elements from a gene linked together. These several regulatory elements can be linked in a way that is substantially the same as in nature or in an artificial way.

A control region in introns and exons may also be 25 involved with regulating the translation of an ob protein, e.g. splicing, processing heteronuclear ribonucleoprotein particles, translation initiation and others described in Oxender, et al. Proc. Natl. Acad. Sci. USA 76:5524 (1979) and Yanofsky, Nature 289:751-758, (1981).

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A control region of this invention is isolated or cloned from a mammalian *ob* gene. It is distinguished from control regions disclosed in the prior art in that it contains a regulatory element of novel or unique nucleic acid sequence for the *ob* gene, a known regulatory element set in a novel or unique nucleic acid sequence context for the *ob* gene, or a few known regulatory elements linked in a novel or unique way for the *ob* gene.

A nucleic acid of this invention can be single stranded or double stranded, DNA or RNA, including those containing modified nucleotides known to one skilled in the art. The complementary strand of an identified sequence is contemplated herein.

In a preferred embodiment, the nucleic acid contains the entire *ob* gene, including the control regions and the amino acid coding region.

In another preferred embodiment, the nucleic acid does not contain the intron between the first two exons of an *ob* gene or portions of the intron.

In yet another preferred embodiment, the nucleic acid contains a control region cloned in a P1 plasmid, such as one of the three P1 vectors (5135, 5136, and 5137) in bacterial strain N8-3529, deposited at ATCC on March 17, 1995 (accession numbers 69761, 69762, and 69763, respectively), e.g. from the sequence 5' to exon 1 in the P1 clones.

In other preferred embodiments, the control region is a promoter capable of initiating the transcription of the *ob* gene.

By "promoter" is meant a DNA regulatory region capable of binding directly or indirectly to RNA polymerase in

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a cell and initiating transcription of a downstream (3' direction) coding sequence. A preferred promoter of this invention contains a sequence from nucleotide -217 to the transcription initiation site of the human *ob* gene or a portion (e.g. at least 60 contiguous nucleotides) of that sequence. A promoter of a DNA construct, including an oligonucleotide sequence according to the present invention may be linked to a heterologous gene when the presence of the promoter influences transcription from the heterologous gene, including genes for reporter sequences such as growth hormone, luciferase, chloramphenicol acetyl transferase, β -galactosidase secreted placental alkaline phosphatase and other secreted enzyme reporters.

Alternatively, the control region is a positive transcription element capable of up regulating or a negative transcription element capable of down regulating the transcription of the *ob* gene, e.g. containing a negative transcription element between nucleotide -978 and -217 of the human *ob* gene or between nucleotide -1869 and -217 of the human *ob* gene.

The control region may contain at least 100, 60, 30, 12, 8 or 6 contiguous nucleotides from the 5' non-coding sequence or an intron of the *ob* gene. In a further preferred embodiment, the control region is from the region 5' upstream of the transcription initiation site of the human *ob* gene, a region between the transcription initiation site of the human *ob* gene and the HindIII site about 3 kb upstream, a region between the first two exons of the human *ob* gene, Seq. ID No. 1, 2, 3 or 4, or a region from nucleotide -217 to -1, -978 to -217 or -1869 to -217 of the human *ob* gene. In yet another

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further preferred embodiment, the contiguous nucleic acid sequence contains a PPRE, RXRE, GRE, insulin response element, C/EBP binding site, Oct-1 binding site, SP1 binding site, AP-1 binding site, AP-2 binding site, serum response element, cAMP response element, or NFkB site, including, but not limited to, those existing in Seq. ID No. 1, 3 or 4.

The ob gene control regions described herein may be used to prepare antisense molecules against and ribozymes that cleave transcripts from the genomic ob sequence, thus interfering or inhibiting RNA processing or translation of the ob gene. Such antisense molecules and ribozymes down regulate the expression of the ob gene.

Antisense nucleic acids of this invention are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule and hybridize to that mRNA in the cell, forming a double-stranded form. Antisense methods have been used to inhibit the expression of many genes *in vitro* (Marcus-Sekura, Anal. Biochem. 172:289-295, 1988; Hambor et al., J. Exp. Med., 168:1237-1245, 1988).

Ribozymes of this invention are RNA molecules possessing the ability to specifically cleave other single-stranded RNA molecules (Cech, J. Am. Med. Assoc., 260:3030-3034 (1988)). Ribozymes capable of modulating the expression of an ob gene may be designed and synthesized with methods known to one skilled in the art such as those disclosed in Stinchcomb, et al. "Method and Reagent for Inhibiting the Expression of Disease Related Genes," WO 95/23225.

The invention also features recombinant nucleic acid comprising a control region of the mammalian ob gene and a nucleic acid sequence (i.e., a reporter sequence), preferably

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inserted in a vector (virus vector or plasmid vector), also preferably in a cell or an organism. The control region and the reporter sequence are operationally linked so that the control region, such as a promoter, is effective to initiate, terminate or regulate the transcription or translation of the reporter sequence. The recombinant nucleic acid may further comprise a transcriptional termination region functional in a cell.

In preferred embodiments, a human *ob* gene control region (e.g. promoter) is selected, the control region and the reporter sequence are inserted in a vector. In further preferred embodiments, the promoter contains the region from the 5' HindIII site to the transcription initiation site of Exon 1 in Figure 9 (i.e. from nucleotide -2921 to -1) or from nucleotide -217 to -1 of the human *ob* gene. Exemplary recombinant nucleic acids are pGL3B-OB1, pGL3B-OB2, pGL3B-OB3 and pGL3B-OB4. In other further preferred embodiments, a positive transcription element or negative transcription element is selected. For example, the negative transcription elements from nucleotide -978 to -217 or from nucleotide -1869 to -217 of the human *ob* gene may be used. Exemplary recombinant nucleic acids are pGL3-OBΔ12 and pGL3-OBΔ5.

By "isolated" in reference to nucleic acid is meant a polymer of 2 (preferably 21, more preferably 39, most preferably 75) or more nucleotides conjugated to each other, including DNA or RNA that is isolated from a natural source or that is synthesized. The isolated nucleic acid of the present invention is unique in the sense that it is not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed

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from its normal cellular context. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment or nucleic acid context. The term does not imply that the sequence is the only nucleotide chain present, but
5 does indicate that it is the predominate sequence present (at least 10 - 20% more than any other nucleotide sequence) and is essentially free (about 90 - 95% pure at least) of non-nucleotide material naturally associated with it. The term does not encompass an isolated chromosome containing an
10 ob gene control region.

By "enriched" in reference to nucleic acid is meant that the specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of the total DNA or RNA present in the cells or solution of interest than in
15 normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two.
20 However, it should be noted that enriched does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased in a useful manner and preferably separate from a library of undefined clones. The term
25 "significantly" here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other nucleic acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there is no
30 DNA or RNA from other sources. The DNA from other sources

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may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes from naturally occurring events, such as viral infection, or tumor type growths, in which the level of one
5 mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

By "purified" in reference to nucleic acid does not
10 require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, e.g., in terms of mg/ml). Individual clones isolated
15 from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially
20 purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the
25 process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the cDNA derived from the native message.

By "recombinant" in reference to nucleic acid is
30 meant the nucleic acid is produced by recombinant DNA

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techniques such that it is distinct from a naturally occurring nucleic acid.

By "enhancer" is meant a DNA regulatory region that enhances transcription. An enhancer is usually, but not always, located outside the proximal promoter region and may be located several kilobases or more from the transcription start site, even 3' to the coding sequence or within the introns of the gene. Promoters and enhancers may alone or in combination confer tissue specific expression.

By "silencer" is meant a control region of DNA which when present in the natural context of the *ob* gene causes a suppression of the transcription from that promoter either from its own actions as a discrete DNA segment or through the actions of trans-acting factors binding to said elements and effecting a negative control on the expression of the gene. This element may play a role in the restricted cell type expression pattern seen for the *ob* gene, for example expression may be permissive in adipocytes where the silencer may be inactive, but restricted in other cell types in which the silencer is active. This element may or may not work in isolation or in a heterologous promoter construct.

By "comprising" is meant including, but not limited to, whatever follows the word "comprising". Thus, use of the term "comprising" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present. By "consisting of" is meant including, and limited to, whatever follows the phrase "consisting of". Thus, the phrase "consisting of" indicates that the listed elements are required or mandatory, and that no other elements may be present. By "consisting essentially

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of" is meant including any elements listed after the phrase, and limited to other elements that do not interfere with or contribute to the activity or action specified in the disclosure for the listed elements. Thus, the phrase

5 "consisting essentially of" indicates that the listed elements are required or mandatory, but that other elements are optional and may or may not be present depending upon whether or not they affect the activity or action of the listed elements.

10 In another aspect, the present invention features a method for identifying agents which modulate or regulate the transcription of an *ob* gene. This method includes (a) providing a system having a control region of an *ob* gene (e.g. human *ob* gene) and a nucleic acid sequence (e.g., a reporter

15 gene) (both of which are preferably inserted in a vector), wherein the control region is transcriptionally linked to the nucleic acid sequence so that it is effective to initiate, terminate or regulate the transcription of that nucleic acid sequence, (b) contacting a candidate agent with the system,

20 and (c) assaying for a measurable difference in the level of transcription of the nucleic acid sequence as an indicant of the candidate's activity. The system may be a cell, an animal such as a mammal, or an *in vitro* transcription system. The preferred cells are eukaryotic cells, including yeast cells

25 and mammalian cells. The recombinant nucleic acid described above may be included in the system to provide the control region and the reporter sequence. An agent that increases the level of transcription of the nucleic acid sequence is an up regulator. An agent that decreases the level of transcription

30 of the nucleic acid sequence is a down regulator. Where an *ob*

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gene has a control region that is also present in a non-ob gene, the control region from equivalent sources may also be used in the screening assay. For example, if a glucocorticoid response element (GRE) is present in an ob gene control
5 region, GREs from other sources may be used to screen for ob gene modulators too.

In a preferred embodiment, the nucleic acid is introduced into a host cell or an organism by either transfection or adenovirus infection and the system includes
10 the cell or the organism. In an even further preferred embodiment, a transgenic animal system is used in the assay.

In another preferred embodiment, the system further includes a transcriptional protein.

By "transcriptional protein" is meant a cytoplasmic
15 or nuclear protein that, when activated, binds a promoter, enhancer or silencer either directly, or indirectly through a complex of proteins to modulate the transcription activity of the promoter. The transcriptional protein may either be endogenous to the cell or expressed from a recombinant nucleic
20 acid transfected into the cell. Examples of transcriptional proteins include, but are not limited to, C/EBP α protein and other proteins that bind to a C/EBP site or Sp1 site, and intracellular receptors.

By "intracellular receptor" is meant an
25 intracellular transcription factor whose activity is regulated by binding of small molecules, including, but not limited to, estrogen receptor (ER), retinoid acid receptors (RAR), retinoid X receptors (RXR), glucocorticoid receptors (GR), progesterone receptors (PR), androgen receptors (AR), thyroid
30 hormone receptors (TR), peroxisome proliferator activated.

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receptors (PPARs, such as PPAR γ) and vitamin D receptors. The intracellular receptor may either be endogenous to the cell or expressed from a recombinant nucleic acid transfected into the cell. Preferred intracellular receptors to be present in the assay include PPAR γ , RXR and PPAR α .

The basal level of the mammalian ob gene expression may be raised up before adding a candidate down regulator to the screening assay.

In a preferred embodiment, the assay is conducted in a mammalian adipocyte cell such as a primary adipocyte cell or a immortalized adipocyte cell. A rat, mouse or a human primary adipocyte cell is used. Mammalian preadipocytes may be used for the assay as well. Exemplary cells include 3T3-F422A, ob 1771, 3T3-L1 and rat primary adipocyte. Any other cells in which the control region is capable of initiating, terminating or regulating the transcription of the reporter sequence may be used.

In another preferred embodiment, the sequence of the control region is used as a guide in selecting potential modulators for screening. For example, if glucocorticoid response elements (GRE), peroxisome proliferator response elements (PPRE), thyroid hormone response elements (TRE), retinoic acid response elements (RARE), retinoid X response elements (RXRE), estrogen response elements (ERE), progesterone response elements (PRE), androgen response elements (ARE), insulin receptor response elements, other transcription regulatory binding sites such as the helix-loop-helix family members including sterol regulatory element binding protein family (SREBP) or its adipocyte expressed homologue ADD-1, CAAT/enhancer binding protein (C/EBP), AP-1,

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AP-2, SP-1, NFkB, Oct-1, serum response elements, cAMP response elements, or growth hormone (GH) response elements are present in this region, compounds known to act through these elements will be selected for screening. Compounds
5 acting on the above mentioned elements can be screened in the assays for ob gene modulators.

In a preferred embodiment, the candidate agent is selected from, but not limited to, the group consisting of estrogen receptor, retinoid acid receptors, retinoid X
10 receptors, glucocorticoid receptors, progesterone receptors, androgen receptors, thyroid hormone receptors, and vitamin D receptors.

In another preferred embodiment, the candidate agent is selected from the group consisting of glucocorticoids;
15 thyroid hormones; thyromimetics; fibrates, free fatty acids and other agonists of PPAR including Di-(2-ethylhexyl)-phthalate, plasticizers and herbicides including 2, 4, 5-trichlorophenoxyacetic acid and leukotriene antagonists; antagonists of PPAR and PPAR subtype selective compounds; RAR
20 selective agonists and antagonists including subtype selective compounds; RXR selective agonists and antagonists including subtype selective compounds; estrogens and other agonists and antagonists of ER; androgens and other agonists and antagonists of AR; progestins and other agonists and
25 antagonists of PR; non-steroid progestins; mineralocorticoids and other agonists and antagonists of MR; insulin; glucose; glucagon; free fatty acids; amino acids; sugars and other secretagogues including biguanides; antidiabetics including metformin and phenformin; pyroglyrides; linoglyrides and
30 benzothenediones; non-steroidal anti-inflammatory drugs;

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prostacyclins; prostaglandins; dihydroepiandrosterone and
stimulators, precursors and derivatives thereof including
Dioscorea and aloe vera, and extracts and compounds derived
therefrom; tumor necrosis factors; cytokines and related
5 signaling molecules; growth factors; fetuin; Amylin agonists
and antagonists; prolactin; niacin; Acepimox and other
nicotinic acid derivatives; triacsin; amphetamines and
derivatives including fenfluramine and dexfenfluramine;
endorphin antagonists; somatostatin; cholecystokinin;
10 bombesin; gastrin; oral anti-diabetic agents; corticotropin
releasing hormone; thiazolidinedione compounds;
adrenocorticotrophic hormones; melanocyte stimulating hormone;
gastric inhibitory peptide; growth hormone agonists and
antagonists; β -adrenergic agonists and antagonists including
15 phenoxybenzamide; fluoxetine; neuropeptide Y and modulators
of its activity or expression; and the gene products of *agouti*
and *GLP-1*.

Candidate compounds of *ob* gene modulators include
but are not limited to those disclosed and referred to in
20 Table 1.

Peptide or small molecule combinatorial libraries
can be used to screen for modulators of *ob* gene expression
(Bunin, B.A.N. Ellman, J. A., *J. Am. Chem. Soc.* 114:10997-
10998 (1992) and references contained therein).

25 Preferred candidate up regulators of an *ob* gene
include PPAR γ antagonist, C/EBP protein agonist, PPAR α
agonist, glucocorticoid, insulin derivative, insulin
secretagogue, insulin sensitizer, and insulin mimetic.

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Preferred candidate down regulators of an *ob* gene include PPAR γ agonist, C/EBP protein antagonist, PPAR α antagonist, glucocorticoid antagonist, and insulin antagonist. A preferred PPAR γ agonist is a thiazolidinedione compound, including, but not limited to, troglitazone (CS-045), pioglitazone (AD-4833), ciglitazone (ADD-3878) and analogs (e.g. WAY-120, 744), BRL 49653 and analogs, englitazone, AD 5075 and darglitazone (CP-86325).

To screen for an agent which modulates the interaction of a ligand with an intracellular receptor, a ligand for the intracellular receptor is included in the assay.

The binding of a transcriptional protein to the *ob* gene promoter and regulatory elements may be measured by techniques known to those skilled in the art, including, but not limited to, mobility shift assay, co-transfection assay, and expression of a reporter gene linked to the promoter.

Applicant discovered that thiazolidinedione compounds reduce the expression of *ob* gene through PPAR γ . Thiazolidinedione compounds are also useful in partially restoring euglycemia in NIDDM patients. They act at both transcriptional and non-transcriptional levels that may mimic or oppose the actions of insulin.

On the one hand, it is known that these compounds act immediately to facilitate the translocation of glucose transporter GLUT4 to the cell membrane where it rapidly increases glucose uptake in treated cells, an effect which cannot be accounted for by transcriptional mechanisms.

On the other hand, these compounds, esp. BRL 49653, have been shown to be ligands for the PPAR γ subtype and can

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act as transcriptional modulators to directly affect the transcription of target genes, e.g. modulating the effects of PPAR γ on the expression of certain genes. For example, BRL 49653 amplifies the suppression of ob gene expression by PPAR γ in primary adipocytes, an effect opposite to that of insulin.

Therefore, thiazolidinedione compounds can exert different effects on a gene or metabolic pathway depending on the combinatorial makeup of the promoter of the gene and whether the effect is transcriptional or non-transcriptional. The screening assay described herein allows one to identify the effect of thiazolidinedione compounds on ob gene expression.

While steroids and steroid analogues may exemplify agents identified by the present invention, Applicant is particularly interested in the identification of agents of low molecular weight (less than 10,000 Daltons, preferably less than 5,000, and most preferably less than 1,000) which can be readily formulated as useful therapeutic agents.

Such agents can then be screened to ensure that they are specific to tissues with pathological conditions related to ob gene expression with little or no effect on healthy tissues such that the agents can be used in a therapeutic or prophylactic manner. If such agents have some effect on healthy tissues they may still be useful in therapeutic treatment, particularly in those diseases which are life threatening.

Once isolated, a candidate agent can be put in pharmaceutically acceptable formulations, such as those described in Remington's Pharmaceutical Sciences, 18th ed., Mack Publishing Co., Easton, PA (1990), incorporated by

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reference herein, and used for specific treatment of diseases and pathological conditions with little or no effect on healthy tissues.

In another aspect, this invention features a pharmaceutical composition capable of modulating the transcription activity of a mammalian (e.g., human) *ob* gene control region, i.e. containing a pharmaceutically effective amount of a modulator (e.g. up regulator or down regulator) of the mammalian *ob* gene control region.

In a preferred embodiment, the composition is held within a container which includes a label stating to the effect that the composition is approved by the FDA in the United States (or other equivalent labels in other countries) for treating a disease or condition selected from the group consisting of obesity, diabetes, infertility, cardiovascular diseases, hypertension, hyperlipidemia, hypercholesterolemia, cachexia and anorexia; or even approval to use the agent by normal humans who wish to change their body weight or other physical conditions by modulating the expression level of the *ob* gene. Such a container will provide therapeutically effective amount of the active ingredient to be administered to a host.

In further preferred embodiments, the composition includes a glucocorticoid, such as, but not limited to, hydrocortisone, triamcinolone or dexamethasone hydrocortisone; insulin, insulin derivative, insulin secretagogue, insulin sensitizer, or insulin mimetic; PPAR γ agonist or antagonist including fish oils, free fatty acids, or thiazolidinedione compounds such as BRL49653 or pioglitazone. Other thiazolidinedione compounds include, but are not limited to,

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troglitazone (CS-045), ciglitazone (ADD-3878) and analogs (e.g. WAY-120, 744), englitazone, AD 5075 and darglitazone (CP-86325).

5 In another aspect, this invention features a method for modulating the expression level of a mammalian *ob* gene by administering to a mammalian cell or a mammal a composition including an effective amount of a modulator (e.g. up regulator or down regulator) of the control region. Other systems (e.g. *in vivo* or *in vitro*, yeast or *Drosophila*)
10 containing a control region of an *ob* gene may be modulated similarly.

In a preferred embodiment, the method further includes step of measuring the transcriptional activity of the control region.

15 In further preferred embodiments, the composition includes an up regulator, e.g. a glucocorticoid, such as, but not limited to, hydrocortisone, triamcinolone or dexamethasone; hydrocortisone; insulin, insulin derivative, insulin secretagogue, insulin sensitizer, or insulin mimetic; PPAR γ antagonist; C/EBP protein agonist; and PPAR α agonist.
20

In another further preferred embodiments, the composition includes a down regulator, e.g. a C/EBP protein antagonist, PPAR α antagonist, glucocorticoid antagonist, insulin antagonist, fish oil, free fatty acid, or PPAR γ agonist including thiazolidinedione compounds such as
25 BRL49653 or pioglitazone. Other thiazolidinedione compounds include, but are not limited to, troglitazone (CS-045), ciglitazone (ADD-3878) and analogs (e.g. WAY-120, 744), englitazone, AD 5075 and darglitazone (CP-86325).

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An effective amount of an agonist or antagonist of PPAR α or PPAR β may also be included in the composition.

In another aspect, this invention features a method for treating a patient with anorexia by administering sufficient amount of a down regulator of human ob gene expression.

In another aspect, this invention features a method for the treatment of cachexia, anorexia or any wasting disease characterized by insufficient food intake or body weight loss, whereby a host (e.g. a mammalian animal or human) is administered with a composition containing a pharmaceutically effective amount of a down regulator of ob gene expression.

In preferred embodiments, the down regulator is a free fatty acid, fish oil, or PPAR γ agonist which includes a thiazolidinedione compound such as BRL49653 or pioglitazone. Other thiazolidinedione compounds include, but are not limited to, troglitazone (CS-045), ciglitazone (ADD-3878) and analogs (e.g. WAY-120, 744), englitazone, AD 5075 and darglitazone (CP-86325). The down regulator may also be a C/EBP protein antagonist, PPAR α antagonist, glucocorticoid antagonist, or insulin antagonist.

In another aspect, this invention features a method for changing the body weight or body fat content of a host by administering to a composition containing a pharmaceutically effective amount of an up regulator or down regulator of ob gene expression. The up regulator may be selected from the group consisting of glucocorticoid, hydrocortisone, triamcinolone and dexamethasone hydrocortisone, insulin, insulin derivative, insulin secretagogue, insulin sensitizer, insulin mimetic, PPAR γ antagonist, PPAR α agonist, and C/EBP

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protein agonist. The down regulator may be selected from the group consisting of PPAR γ agonist, thiazolidinedione, BRL49653 and analogs, pioglitazone, troglitazone (CS-045), ciglitazone (ADD-3878) and analogs (e.g. WAY-120, 744), englitazone, AD 5075, darglitazone (CP-86325), free fatty acid, fish oil, C/EBP protein antagonist, PPAR α antagonist, glucocorticoid antagonist, and insulin antagonist.

In another aspect, this invention features a method for treating an overweight patient having a body weight more than about 10% or about 20% in excess of the ideal body weight by administering a composition containing a pharmaceutically effective amount of an up regulator of *ob* gene expression.

In another aspect, this invention features a method for helping a person having a functional *ob* gene to control his or her body weight by administering a composition containing a pharmaceutically effective amount of a modulator of human *ob* gene expression.

By "a functional *ob* gene" is meant an *ob* gene encoding an *ob* protein having substantially the same biochemical activity of the wild type *ob* proteins disclosed in Zhang et al., Nature 372:425-432, 1994, including, but not limited to, the wild type *ob* genes disclosed in Zhang et al., id. A functional *ob* gene may have some differences from the wild type *ob* genes disclosed in Zhang et al., id., yet these differences do not significantly change the biochemical activity of the *ob* protein expressed therefrom. Also included is the case where one allele of *ob* is mutated, leaving only one functional copy of the *ob* gene whose expression is subject to modulation.

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In yet another aspect, this invention features a composition and method to use this composition to change the body weight or body fat content of an animal, including, but not limited to, a mammalian animal for veterinary or agricultural purposes; this composition comprises an effective amount of a modulator of *ob* gene expression.

The present invention also relates to the isolation and identification of the promoter and other regulatory elements of other genes in the fatty acid metabolic pathways using methods described herein for the *ob* gene. These genes include, but are not limited to, *fat*, *tub*, *db* (diabetics), *agouti*, glucagon-like protein-1, neuropeptide-Y and *fatp* (fatty acid transfer protein). The discoveries of control regions for these genes allow for the screening of agents that specifically influence these genes' expression and thence for construction or design of other modulators of such genes' expression. Such discovery will also allow identifying therapeutic agents and using these agents to treat diseases and conditions affected by these genes and/or these genes' product, such as, but not limited to, obesity, cardiovascular diseases, diabetes and anorexia.

Other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a graph which shows body weights of rats upon treatment with hydrocortisone. Adult male rats received once-daily subcutaneous injections of hydrocortisone (100 μ g/g body weight) for the indicated number of days. Control

Identification
of nucleotides
of other members
of the
Nuc family
in nucleic
acids.
Such discovery
allows for
discovery
construction &
identification of
modulators of
ob gene
Nuc family.

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animals received saline only. Body weights were recorded at regular intervals and are expressed as a percentage of pretreatment (day 0) body weight. Values represent the mean \pm SD of 4 animals/group.

5 Figure 2 is a graph which shows food consumption upon treatment with hydrocortisone. Adult male rats (n=4/group) were treated as described in Figure 1. Total food consumption of each treatment group was measured at regular intervals and is expressed as a percentage of the food intake
10 of a group of sham-treated controls.

 Figure 3 is a graph which shows *ob* mRNA level in adipose tissue with treatment with hydrocortisone. Adult male rats (n=4/group) were treated as described in Figure 1. Adipose tissue was isolated, RNA was extracted and *ob* and β -
15 actin mRNA levels were measured as described below. Values represent the mean \pm SD of 4 animals and are expressed in relative absorbance units (R.A.U.) taking the pre-treatment values as 100%.

 Figure 4 is a graph which shows body weight gain (A)
20 an adipose tissue's *ob* mRNA levels (B). Adult male rats (n=4 animals/group) received once-daily subcutaneous injections of hydrocortisone at the indicated doses for 20 days. Control animals received saline only.

 Panel A: Body weights were recorded at the beginning
25 and end of the experiment and are expressed as percentage of pre-treatment (day 0) body weight.

 Panel B: At the end of the experiment adipose tissue was isolated, RNA extracted and *ob* and β -actin mRNA levels measured as described in materials and methods. Values are

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expressed in relative absorbance units (R.A.U.) taking the controls as 100%.

Figure 5 is a graph which shows body weight, food consumption (A) and adipose tissue's *ob* mRNA levels (B).

5 Panels A&B: Adult male rats (n=3 animals/group) were treated for 4 days with vehicle (CON), hydrocortisone (HC; 100 μ g/g body weight/day), triamcinolone (TRIAM; 20 μ g/g body weight/day) or dexamethasone (DEXA; 3.7 μ g/g body weight/day). Body weight and food consumption were recorded at the end of
10 the experiment and are expressed as percentage of the controls (Panel A). Adipose tissue was isolated, RNA extracted and *ob* and β -actin mRNA levels were measured as described below (Panels B). Values are expressed in relative absorbance units (R.A.U.) taking the controls as 100%.

15 Adult male rats (n=3 animals/group) were sacrificed 24 hr after a single injection of dexamethasone (DEXA; 3.7 μ g/g body weight/day) or vehicle (CON). 10 mg of total RNA extracted from individual animals was pooled and subjected to electrophoresis, transferred to a nylon membrane and
20 hybridized consecutively to labeled *ob* (top panel) or β -actin (bottom panel) cDNA as described below. The position of the 18S and 28S rRNA bands are indicated on the right of the top panel.

25 Figure 6 is a restriction map of clones 1B41 and 1F41. Coding sequence has been localized to the unique 5' XhoI-HindIII 3' fragment indicating that clone 1B41 has more than 5 Kb of 5' flanking sequences.

Figure 7 is a graph which shows the level of *ob* gene transcription after food consumption or insulin injection.

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Figure 8 is a restriction map of clone 1B41 showing schematically the approximate positions of ATG start codon for human ob gene, primers ob1, ob7 and P1, and the sequenced region represented by Seq. ID No. 3.

5 Figure 9 is a map showing the 5' upstream of the human ob gene. (a) is a restriction map wherein B=BamHI, E=EcoRI, H=HindIII and X=XhoI. (b) shows the location of a control region. (c) identifies regions that have been sequenced. (d) shows the location of the 1B41 clone. (e)
10 shows the location of the EcoRI subclone of the 1B41 clone. (f) shows the location of the HindIII subclone of the P1 clones. (g) shows the location of the EcoRI subclone of the P1 clones. (h) is a scale showing the size of this map.

 Figure 10 (a) is a genomic map of the human ob gene.
15 The gene is shown in 5' to 3' orientation at the top of the diagram and is drawn to scale. Exons are denoted by black rectangles and introns by a solid line. Restriction sites for Bam HI, EcoRI, and HindIII are indicated by their first letter. Transcription initiation sites are indicated by the
20 arrow, whereas the location of the ATG start-codon and TGA stop-codon are indicated. The regions encompassed in the λ phage and 5135 P1 clones are indicated at the bottom. 10(b) is a map showing the structure of the human ob cDNA clone phob6.1. The different exons are highlighted. The
25 approximate location of the various oligonucleotides used in the project are indicated at the bottom.

Figure 11 is a graph which shows the levels of ob mRNA and plasma glucose after insulin injection and food consumption.

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Figure 12 is a graph which shows the levels of ob mRNA after insulin injection when plasma glucose levels were maintained at either high or low levels.

Figure 13 is a graph which shows the levels of ob mRNA and actin mRNA in rat primary adipocytes after insulin treatment.

Figure 14(a) is sequences showing ob gene transcription initiation sites in human and rat as determined by 5'-RACE and primer extension; 14(b) is an autoradiograph showing the result of primer extension.

Figure 15(a) is a diagram showing the locations of Sequence I.D. Nos. 1, 2 and 3; 15(b) is a diagram showing the locations of ob gene promoter, Exon 1, Intron 1, Exon 2 and translation initiation ATG codon.

Figures 16 (a), (b), (c) and (d) are diagrams showing schematic organization of plasmids pGL3B-OB1, pGL3B-OB2, pGL3B-OB3 and pGL3B-OB4, respectively.

Figure 17(a) is a diagram showing the difference in construction between pGL3B-Basic and pGL3B-OB1; 17(b) is a graph showing luciferase activity in 3T3-L1 cells transfected with pGL3B-Basic or pGL3B-OB1 with or without insulin treatment.

Figure 18(a) is a diagram showing the constructs of pGL3B-Basic, pGL3B-OB1 and pGL3B-OB2; 18(b) is a graph showing normalized luciferase activity of the pGL3B-OB1 construct containing 3 kb of regulatory sequence of the human ob gene after transfection in rat primary adipocytes, 3T3-L1, CV-1 and COS cells; 18(c) is a graph showing normalized luciferase activity in rat primary adipocytes and 3T3-L1 cells transfected with pGL3B-Basic, pGL3B-OB1, or pGL3B-OB2. It

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shows that 217 bp of the 5' flanking region is sufficient to drive the expression of luciferase gene in transfected rat primary adipocytes and 3T3-L1 cells.

Figure 19(a) is a graph showing normalized luciferase activity in rat primary adipocytes transfected with pGL3B-Basic, pGL3B-OB1 or pGL3B-OB2 and with or without a C/EBP- α expressing plasmid, pMSV-C/EBP (8 μ g); 19(b) is a graph showing normalized luciferase activity in 3T3-L1 cells transfected with pGL3B-Basic, pGL3B-OB1 or pGL3B-OB2 and with or without a C/EBP- α expressing plasmid, pMSV-C/EBP (2 μ g); 19(c) is a graph showing normalized luciferase activity in rat primary adipocytes transfected with pGL3B-OB1 and increasing amount of C/EBP α expression vector. The amounts of cotransfected C/EBP α expression vector were 0, 2, 4 and 8 μ g.

Figure 20 (a), (b) and (c) are graphs showing adipose tissue endogenous ob mRNA levels in rats after treatment with BRL 49,653 (BRL; 10mg/kg/day for 7 days), fenofibrate (FF; 0.5% w/w for 14 days), or a diet enriched in fish oils (FO; 20% of total caloric intake for 3 months). Results are expressed as the mean \pm SD. Significant differences from control values (CON), as determined by Student's t-test ($p < 0.005$), are indicated by an asterisk.

Figure 21 (a) is a graph showing endogenous ob mRNA levels in rat primary adipocytes after treatment with BRL 49,653 (100 μ M, 24 hr) or fenofibric acid (250 μ M, 24 hr). Results are normalized to γ -actin levels. 21(b) is a graph showing normalized luciferase activity in rat primary adipocytes transfected with pGL3B-OB1 (with 5 μ g of pSG5-cgPPAR γ expression vector or the empty pSG5 expression vector

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in the presence or absence of 10 μ M BRL 49,653 or 10 μ M pioglitazone (PIO)).

Figure 22 is a graph showing the effect of BRL49653 on food intake in rats. Rats were administered either 0, 5, 10 or 20 mg/kg/day of BRL49653 and the effect on food intake was recorded daily.

Figure 23 is a graph showing the dose-dependent of BRL49653 on ob mRNA levels. Male rats were administered either 0, 1, 2 or 5 mg/kg/day of BRL49653 for 7 days. Adipose tissue RNA was isolated and mRNA levels quantified. The mean \pm SD for 4 animals is shown.

Figure 24 is a graph showing the promoter activity of the pGL3-OB1 (2 μ g) construct in 3T3-L1 preadipocytes. Luciferase activity was determined in cells cotransfected with either 2 μ g of pSG5-cgPPAR γ or the empty pSG5 expression vector in the presence or absence of 10 μ M BRL 49,653. Cells were exposed to BRL 49,653 for 24 hours. The mean of 4 points is shown.

Figure 25 (a) is a schematic representation of the various human ob gene promoter - luciferase constructs used in the assay. 25 (b) is a graph showing luciferase activity in 3T3-L1 preadipocytes driven by various nested deletions of the human ob promoter. Luciferase activity was determined in cells cotransfected with either 1 μ g of the pSG5-cgPPAR γ or the empty pSG5 expression vector. Results represent the mean of five points.

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DETAILED DESCRIPTION OF THE INVENTIONI. Cloning the ob Gene Control Regions

The present invention embodies the realization that the precise genetic elements which are responsible for ob gene expression can be isolated away from ob gene open reading frame (i.e., amino acid coding sequences) and employed to assay for agents that modulate ob gene expression.

The present invention describes that the human ob gene has two introns and three exons (see Figure 9). The novel nucleic acid sequences of the present invention comprise the ob gene control region such as (1) sequences which provide a positive promotion of transcription, i.e., promoters and enhancers; or (2) sequences which provide a negative regulation of transcription, e.g., silencers. Other mammalian ob gene control regions may be isolated by the methods described below and by hybridization of other mammalian DNA libraries with probes derived from the human ob gene control regions.

Oligonucleotide primers

The oligonucleotides used for various aspects in this application are listed below (whereas N1 = G, A, or C; and N = G, A, C, or T):

1F:	5'-ATG CAT TGG GGA ACC CTG TGC GG-3'
25 140R:	5'-TGT GAA ATG TCA TTG ATC CTG GTG ACA ATT-3'
217R:	5'-GAG GGT TTT GGT GTC ATC TTG GAC-3'
562R:	5'-CCT GCT CAG GGC CAC CAC CTC TGT CG-3'
anchored-T:	5'-TTC TAG AAT TCA GCG GCC GC(T) ₃₀ N ₁ N-3'
AP1:	5'-CCA TCC TAA TAC GAC TCA CTA TAG GGC-3'
30 AP2:	5'-ACT CAC TAT AGG GCT CGA GCG GC-3'

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pdv34R: 5'-GCC ACA AGA ATC CGC ACA GGG TTC CCC ATG C-3'
 RACE1: 5'-CTC TTA GAG AAG GCC AGC ACG-3'
 RACE2: 5'-CGC GGG CTC GAG AAG GTC AGG ATG GGG TGG AGC-3'
 SMFOR: 5'-CGC AGC GCC AAC GGT TGC AAG GC-3'
 5 SMREV: 5'-GCC TTG CAA CCG TTG GCG CTG CG-3'
 SMREV2: 5'-CGC GGG AAG CTT GCC TTG CAA CCG TTG GCG CTG CG-3'
 MUT1a 5'-GAG CCT CTG GAG GGA CAT CA-3'
 MUT2a 5'-TGG CGT CTT CCA TGG GGT CT-3'
 10 CEBPfor 5'-GCC TGC GGG GCA GTT AAA AAA GTT GTG ATCG-3'
 CEBPrev 5'-CGA TCA CAA CTT AAA AAA CTG CCC CGC AGG-3'
 OB/S1 5'-GCT TCT TGG GCC TTG CAA CCG TTG GCG CTG CGA TTC
 CTA CGG GGC TCC ATG CCT GC-3'

15 Cloning mouse ob cDNA

A mouse ob cDNA fragment spanning nucleotides +50 to +659 was cloned from mouse adipose tissue by reverse transcription and PCR-amplification (sense primer, 5'CCA AGA AGA GGG ATC CCT GCT CCA GCA GC - 3' anti-sense primer, 5'-CCCTCT ACA TGA TTC TTG GGT ACC TGG TGG CC-3') (Zhang et al., Nature 372:425-432, 1994). The resulting PCR-fragment was digested with BamHI and KpnI and cloned into the BamHI and KpnI site of pBluescript KS to generate pmob.1. Sequence analysis of pmob.1 revealed complete identity to the reported mouse ob cDNA sequence (Zhang et al., Nature 372:425-432, 1994).

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Cloning human ob cDNA

A human adipose tissue λ gt11 library was next screened with the complete mouse ob cDNA as a probe. Duplicate filters were prepared and hybridized with 32 P-labeled (random priming; Boehringer Mannheim) BamHI-KpnI fragment of mouse ob cDNA clone pmob.1. After hybridization filters were washed in 0.2 x SSC and 0.1% SDS for 10 min at room temperature (about 20-25°C) and twice for 30 minutes in 1 x SSC, 0.1% SDS at 50°C and subsequently exposed to X-ray film (X-OMAT-AR, Kodak). Several positive clones which gave signals on both duplicate filter lifts were obtained and one of them, ob 6.1 was characterized in detail. A 1.6 kb EcoRI fragment of this clone starting about 90 bp upstream of the ATG start codon and extending downstream into the 3'UTR sequence was subcloned into the EcoRI site of pBluescript SK-, to generate phob 6.1. The sequence of the 5'UTR region is 5'- GGC CCC TGA CCA CCA GGA ACT GAA CCT TGA TGC GTC CCT CCA ACT GCC CAG CCG CAG CTC CAA GCC AAG AAG CCC ATC CTG GGA AGG AAA ATG -coding region -3'. Sequence analysis of phob 6.1 confirmed it as being the human homologue of the mouse ob cDNA (Zhang et al., *Nature* 372:425-432, 1994).

Isolating human genomic ob clones

The genomic library was derived from female leucocyte DNA partially digested with Sau3A and inserted into λ DASHII arms. The library contains 5×10^5 independent recombinants and has an insert size between 15-20 kb.

For the initial screening, a 32 P-labeled (random priming; Boehringer Mannheim) unique BamHI-KpnI fragment of mouse ob cDNA clone pmob 1 was used as a probe. Filters were

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washed in 2 x SSC, 0.1% SDS for 10 minutes at room temperature and twice in 0.1 x SSC, 0.1 % SDS at 65°C for 30 minutes. During this round of screening 8 positive plaques were identified.

5 In the first purification step, the ³²P labeled (random priming: Boehringer Mannheim) 1.6 kb insert released by Eco RI from phob 6.1 was used as a probe, and the treatment of the filters was identical as in the initial screening.

10 Two genomic phage clones were retained and they were termed 1B41 and 1F41. Both clones were again positive upon the second round of purification and were verified to be pure. Clone 1B41 contains an insert of approximately 17 kB, whereas 1F41 has an insert of 13 kb which overlaps to a large extent with clone 1B41. These clones were further characterized by
15 restriction analysis with the restriction enzymes EcoRI, Hind III, and Xho I, and a restriction map is presented in Figure 6.

 In order to further characterize these clones a set of PCR reactions were performed. Initially we verified
20 whether the entire coding region was contained in our genomic clones. PCR amplifications using the 1F/217R primers resulted in the appearance of a 102 bp band when either genomic DNA, the 1B41 and 1F41 genomic clones, or the phob 6.1 cDNA were used as template, suggesting that both primers were localized
25 in a single exon. When PCR reaction was carried out with the 1F/562R primers, a 2.5 kb band was amplified from human genomic DNA and from the 1B41 and 1F41 genomic clones.

 However, amplification on the phob 6.1 cDNA with 1F and 562R primers resulted in the appearance of a 447 bp
30 fragment consistent with the presence of an intron in the

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region confined between 217R and 562R. These data suggested that the 1B41 and 1F41 clones contained the entire coding region of the human ob gene as well as intron genomic sequences.

5 The 1B41 and 1F41 clones hybridized with oligonucleotide 1F, which covers the ATG start codon and with oligonucleotide 562R, localized in the 3' region of the coding sequence indicating that the entire coding sequence was contained in these clones. Further, sequencing of 1B41 in the
10 5' direction using oligonucleotides ob 1 (5' CATTTCCTTCCCAGGATG 3'), ob7, and P1 has yielded sequence information diverging from the cDNA sequence of clone phob 6.1 (no homologous sequence is found in Genbank) (from 5' to 3', see sequence ID No. 3).

15

Cloning the entire human ob gene in P1 plasmid

In order to isolate genomic P1 plasmid clones containing the entire human ob gene, the primer pair 1F/140R were used to amplify a 140 bp probe with the phob 6.1 plasmid
20 as a template. This fragment was then used to screen a P1 human genomic library. P1 library is from human foreskin fibroblast (Sternberg et al., New Biologist 2:151 (1990); Trends in Genetics 8(1), January 1992).

A number of hybridizing clones (about 100) yielded
25 from the primary screen of the P1 library. The screening can be repeated with the novel 5' flanking sequence from the 1B41 clone with the primer pair ob 1 and kenobe (5' TGGGTGAGTACCATAATCGC 3') to identify clones containing the ob gene 5' flanking sequences. Primer pair 1F and 140R was used
30 to generate a probe to screen the P1 clones.

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Three positive clones were isolated and termed 5135, 5136, and 5137. All three clones were shown to hybridize with the following oligonucleotides 1F, ob 1, 562R and 140R as well as kenobe oligos at the extreme 5' sequence obtained from the 1B41 clone, thus demonstrating that the sequence 5' to the coding region of the ob gene is contained in these P1 clones. Standard molecular biology techniques were used to further characterize the 5' regions of the ob gene to locate control regions, such as detailed restriction analysis, genomic sequencing of the 5' regions of the ob gene contained within the P1 clones, and primer extension and S1 mapping analysis of human adipose tissue.

Determining the transcription initiation site of the ob gene

15 5'-RACE

The Marathon cDNA amplification kit (Clontech) was used for 5'-Rapid Amplification of cDNA Ends (RACE) to obtain the sequence of the 5' untranslated region (5'-UTR) of the human ob gene transcript. The 5'-RACE was performed on total RNA (1µg) from several independent human white adipose tissue samples and on double stranded cDNA derived from human adipose tissue (Clontech). The anchored-T primer included in the kit or the ob-specific primer 562R were used to prime first strand synthesis on adipose tissue RNA and second strand synthesis was performed according to the instructions provided by the manufacturer. PCR reaction products were recovered, ligated into the TA cloning vector pCRII (InVitrogen), and sequenced.

Total human white adipocyte tissue (WAT) cellular RNA was prepared by the acid guanidinium thiocyanate/phenol

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chloroform method (Choeczynski, et al., Analytical Biochemistry 162:156-159, 1987)

First-strand cDNA synthesis was performed in parallel reactions, each using 1 μ g of total RNA isolated from human white fat as template. One reaction utilized an anchored-T primer to prime first strand synthesis. A second reaction utilized a primer specific for human ob (562R) for first strand synthesis.

An anchored-T primer, included in the Clontech kit, was used to prime first strand synthesis. After synthesis of double-stranded cDNA and anchor ligation, polymerase chain reaction was carried out using the following primer sets: AP1/140R, AP1/RACE1 and AP1/RACE2.

The 5' ends of these primers are located at +140bp (140R), +215bp (RACE2), and +347bp (RACE1) relative to the ATG start codon of the open reading frame of human ob gene. The anchor primer AP1 is provided in the Clontech kit. A fraction of the primary 5'-RACE product derived from this PCR reaction was run on a polyacrylamide gel and products were visualized by staining with ethidium bromide. A band of about 360bp was obtained.

5'-RACE was also carried out using double stranded cDNA derived from human fat tissue obtained from Clontech (Part #7128-1). The anchors included in the Marathon kit were ligated to this cDNA and PCR amplification and cloning carried out as described above. The products of the PCR step were separated on an agarose gel and visualized with ethidium bromide. The major bands were recovered from a low melting point agarose gel and ligated into the TA cloning vector pCRII (InVitrogen).

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A parallel set of ligations were performed using the 5'-RACE PCR product without purification. The clones obtained were sequenced using the 140R primer.

Secondary PCR was carried out on aliquots of the
5 primary 5'-RACE product using the primer sets AP1/217R, AP2/217R or 1F/217R. The primer AP2 anneals to sequences located within the 5'-RACE anchor and is nested relative to the AP1-binding sequence. A product of about 360bp was recovered from both the AP1/217R and AP2/217R PCR reactions
10 and a product of about 100bp was recovered from the 1F/217R PCR reaction.

The product from the 1F/217R PCR reaction was the size expected from the human *ob* sequence and comigrated with the product of parallel PCR reactions carried out using
15 1F/217R and either the human *ob* cDNA clone phob6.1 or the human genomic clone 1B41 as template. Therefore, the primary 5'-RACE product contains authentic human *ob* sequence and the full length human white fat mRNA contains a 5' untranslated region of about 260bp.

20 The product of the AP2/217R PCR reaction was ligated into the vector pCR-Script SK(+) (Stratagene) using the methods described by the manufacturer. The cloned inserts were sequenced on both strands. The AP2/217R PCR product was also subjected to direct DNA sequencing using cycle sequencing.

25

A. 5' RACE with RNA

Sequence was obtained from four independent 5'-RACE clones (Clones 1-4; Table 1) using a sequencing primer located within the coding region of human OB (140R). The sequences are
30 listed in Table 2.

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Sequences shown above are from the region between the AP1 5'-RACE primer and the ATG start codon (bold) for the initiating methionine of human ob protein. The underlined regions indicate sequences that diverge from the genomic sequence (see Table 4 for comparison).

Clones 1, 2 and 3 were obtained using primers 140R and AP1 for PCR. Clone 4 was obtained using primers RACE1 and AP1.

10 B. 5' RACE with cDNA

A second set of 5'-RACE reactions were carried out using human adipose tissue double-stranded cDNA (obtained from Clontech) as starting material. Sequence was obtained from three clones (clones 5-7; Table 3). These sequences were identical to one another and to the 5'-RACE sequences obtained from the independent tissue source shown above. These clones were 3 base pairs shorter than the longest 5'-RACE clone obtained using human adipose total RNA as a starting material.

Sequences shown above are from the region between the AP1 5'-RACE primer and the ATG start codon (bold) for the initiating methionine of human ob protein. The underlined regions indicate sequences that diverge from the genomic sequence (see Table 4 for comparison).

These clones were obtained using the primers 140R and AP1 for PCR.

The sequences of all seven clones diverge from the genomic sequence 26 bp 5' from the initiating ATG of the human ob reading frame (Table 4).

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Genomic Clone (2) is shown relative to the sequence of human genomic DNA in this region. Regions of sequence identity are indicated ([]), the novel sequence is underlined. The following experiment was carried out to map the 5' exon on human genomic P1 clones.

Primer extension

The oligonucleotide pdv34R was ³²P-labeled and used for the primer extension reaction at 10⁵ dpm per 50 µg adipose tissue total RNA from different subjects in a final reaction volume of 100 µl. The reaction mix was precipitated and the primer extension reactions were carried out using standard methodologies with a mixture of 1.25 Units of AMV reverse transcriptase (BRL) and 100 Units MMLV reverse transcriptase (BRL). Reaction products were phenol/chloroform extracted, precipitated, dissolved in formamide loading buffer and run on a 10% denaturing acrylamide gel. A sequencing reaction of an ob cDNA clone with the same primer was run in parallel to map the position of the extension products.

Figure 14 shows human and rat ob gene transcription initiation sites as mapped by 5'-RACE and primer extension.

S1 analysis

50,000 cpm of a 5' ³²P-labeled, gel-purified oligonucleotide probe OB/S1 was annealed (14 hr, 30°C) to 50 µg adipose tissue total RNA from different subjects in 20 µl hybridization buffer. A 10 µl aliquot of the annealing reaction was subjected to S1 nuclease digestion according to the manufacturer's protocol (Ambion) and the reaction products analyzed on a 10% denaturing gel. A ³⁵S-labeled 10-nucleotide

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ladder was used as a size standard. This method confirmed the most 5' start site as identified by primer extension assay.

Mapping the 5' exon of the human ob gene in the P1 clones

5 A. Identifying and isolating the 5' intron on human genomic P1 clones by PCR

Two oligonucleotides, SMFOR and SMREV, were synthesized based on the sequence obtained from 5'-RACE. SMFOR and SMREV are reverse complements of one another.

10 Extended PCR was carried out on three human genomic P1 clones (5125, 5126, 5127) using SMFOR and 140R as primers.

15 An identical PCR product of approximately 10-12 kb was obtained using all three P1 clones. Amplification of this band required the presence of both primers and template. No product was obtained when the human genomic λ clone 1B41 was used as template.

20 This data indicates that an intron of approximately 10-12 kb is present in the primary transcript of the human ob gene. The exon within which the SMFOR/SMREV sequence is located ("5' exon") is not contained in the genomic clone 1B41 but is present in the three P1 clones. All three P1 clones hybridized with oligos from the 5' (1F) and 3' (562R) extremes of the coding sequence as well as the oligo SMFOR derived from the 5' RACE, and hence contain the transcription initiation site of the ob gene.

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B. Locating the 5' exon on the P1 clones by restriction mapping

To localize the 5' exon within each of the three P1 clones, the clones were digested with either BamHI, EcoRI, HindIII or NotI. The restriction digests were separated on agarose gels, transferred to nitrocellulose, and probed by Southern hybridization using [³²P]-labeled SMFOR as a probe.

A single major band was detected in each digest. The sizes of the hybridizing bands were identical for all three P1 clones in the EcoRI (approximately 3 kb), HindIII (approximately 7.2 kb), and NotI (>20 kb) digests. The sizes of the hybridizing bands were different for each of the three clones when digested with BamHI (5125 =11 kb; 5126 =14 kb; 5127 =12 kb). The BamHI results indicate that the 5' exon is located within approximately 11-14 kb of one end of each of the P1 inserts.

The EcoRI fragment and HindIII fragment from the P1 clone containing the 5' exon were subcloned into pBSII-SK+, respectively (see Figure 9 for the location of the EcoRI and HindIII fragments).

Sequence obtained from the HindIII subclone using the M13 -20 flanking primer (the HindIII site is underlined):

5' AAGCTTCTTT AAGGATGGAG AGGCCCTAGT GGAATGGGGA GATTCTCCG
GGAGAAGCGA TGGATGCACA GTTG -3'

Sequence obtained from the HindIII subclone using the T3 flanking primer (the HindIII site is underlined and a BamHI site is double underlined):

5' - AAGCTTTAGC TAGTCTGAGT CCTCTCCCTA TACACATTCT CCTGTGGGAT
CCCTCCTG -3'

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This sequence is identical to a region of genomic sequence localized within the 10-12 kb intron approximately 6.4 kb 5' of the initiating ATG. The location and orientation of this HindIII clone is shown in Figure 9.

5 Sequence obtained from the EcoRI subclone using an M13 -20 primer (the EcoRI restriction site is underlined):
 5'- GAATTCCTAC CCGCAGAGCA AGGCAATGTC TGGGACTGAG ACTGATCACT
 TGCATCTGCG TCTCTCCTAN NCCCACTTT ATCTCCTTCA GACTGGGGTG
 GGACATCTGA TCTTTGGG -3'

10 Sequence obtained from the EcoRI subclone using a T3 primer (the EcoRI restriction site is underlined):
 5'- GAATTCAAAA CTTTATAGAC ACAGAAATGC AAATTCCTG TAATTTNNCC
 GTTGAGAACT ATTCTTCTTT -3'

15 The following sequence was obtained from both the HindIII subclone and the EcoRI subclone using the SMREV primer:

5'- ACTGCCCCGC NGGCCCCGGC GCATTCTAG CGCCAGCTCC CGCCCCGCCC
CTTCAGGTAG CGACAGTGCC GGGCGGCTGC TAGCCCTGGG CCCGAGTGT
 GCACCTCGCG GGGCCTCGAG GGAGGGC -3'

20 The letter "N" indicates an ambiguous base. The region upstream of the 5' exon contains a control region regulating ob gene expression. Two SP1 binding sites are double underlined.

25 Figure 15 shows the splicing pattern in human genomic ob gene. Transcription starts at Exon 1, goes through Intron 1 to reach Exon 2. The translation start codon ATG is located inside Exon 2.

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Physical map of the human ob gene.

The results indicated above were used to generate a physical map of the human ob gene locus (Figure 9). Three exons and two introns exist within the primary transcript of the human ob gene. Promoter and control regions are present in the region immediately upstream of the 5' exon within the HindIII subclone. Addition genetic control regions may be present within the 5' intron.

As shown in Figure 15, Sequence I.D. No. 1 represents 294 bp of the proximal promoter region, upstream of the transcriptional initiation site as determined by primer extension. A C/EBP binding site (5' TTGCGCAAG3') and an XhoI site (5'CTCGAG3') are located within Sequence I.D. No. 1. Sequence I.D. No. 2 represents the entire sequence of Exon 1. Sequence I.D. No. 3. represents the entire sequence of Intron 1, starting at the nucleotide 3' to Exon 1, and extending to the nucleotide 5' to Exon 2. Seq. I.D. No. 4 starts at the HindIII site immediately upstream of Exon I and ends at sequence -1, the nucleotide 5' next to the transcription initiation site. There are PPRE half sites, GRE sites, and a TATA box sequence (5' TATAAGA 3') in Seq. I.D. No. 4.

The human ob gene's three exons cover approximately 15 kb of genomic DNA. The entire coding region is contained in exons 2 and 3, which are separated by a 2 kb intron. The first small 30 bp untranslated exon is located > 10.5 kb upstream of the initiator ATG codon. 3 kb of DNA upstream of the transcription start site has been cloned and characterized.

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Delineating ob gene promoter and other control regions

Segments of DNA from the 5' upstream region of the transcription initiation sites were assayed for their transcription regulation activities.

5 A. Construction of ob promoter-luciferase reporter vectors

To test the activity of the human ob promoter, several reporter constructs were made. A 7 kb HindIII fragment of P1 clone 5135 that hybridized to oligo SMPOR, was
10 subcloned into the HindIII site of pBluescript (Stratagene). From this construct a fragment of about 3kb in length, containing sequences from about -3 kb (5' HindIII site) to +31 relative to the transcription start site, was amplified by PCR with Vent polymerase using the HindIII subclone as template.
15 The primers used were M13(-20) (5'-GTAAAACGACGGCCAGT-3') and SMREV2 (containing a HindIII site). The PCR product was digested with HindIII and ligated into the HindIII site of the promoterless luciferase reporter vector pGL3-Basic (Promega) to generate pGL3-OB1 (5' HindIII site to +31) and sequenced to
20 confirm orientation.

To avoid any errors introduced by the PCR step, an approximately 2.8 kb Asp718 fragment of pGL3B-OB1 was replaced by an equivalent fragment isolated from the 7 kb genomic HindIII clone in BlueScript. This plasmid was designated
25 pGL3B-OB3 and represents a more authentic version of pGL3-OB1.

A third luciferase reporter vector, was constructed by digesting pGL3B-OB1 with Asp718 (or KpnI which is an isoschizomer of Asp718) and religating the Asp718(KpnI)-HindIII subfragment, spanning from -217 to +31, into the

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gel-purified vector backbone. This reporter vector was designated pGL3B-OB2 or pGL3-OB2.

5 A fourth luciferase reporter vector, containing -170 to +31, was constructed by digesting pGL3B-OB1 with XhoI and religating into the gel-purified vector backbone. This plasmid was designated pGL3B-OB4.

10 The orientation and construction of pGL3B-OB1, pGL3B-OB2, pGL3B-OB3 and pGL3B-OB4 are shown in Figure 16(a)-(d). In this application, pGL3B-OB1 and pGL3-OB1 are interchangeable, so are pGL3B-OB2 and pGL3-OB2, pGL3B-OB3 and pGL3-OB3, and pGL3B-OB4 and pGL3-OB4.

15 The C/EBP α mutant construct pGL3-KOB1 was constructed using the mismatch PCR technique. Briefly, an oligonucleotide corresponding to sequences 5' to the Asp 718 in pGL3-OB1 (MUT1a) and a 3' oligo outside the multiple cloning site (MUT2a) and two additional oligos encompassing the C/EBP site (CEBPfor and CEBPrev) were synthesized. The first PCR step involved amplification with pGL3-OB1 as template and the primer pairs CEBPrev + MUT1a in one reaction and CEBPfor + MUT2a in a second reaction. The gel isolated products were pooled and reamplified with MUT1a + MUT2a primers. The resultant PCR product was digested with NcoI and Asp718 and subcloned into NcoI and Asp718 digested pGL3-OB1 and sequenced to confirm the mutant sequence. The pMSV-C/EBP α (Christy, et al., Genes and Development 3:1323-35, 1989) expression vector is described elsewhere.

20 Transfections were performed using either standard calcium phosphate precipitation techniques (Schoonjans, et al., J. Biol. Chem. 270:19269-19276, 1995) or electroporation for primary adipocytes (Quon, et al., Biochem. Biophys. Res.

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Commun. 194:338-346, 1993). Luciferase assays were carried out exactly as described previously (Schoonjans, et al. J. Biol. Chem. 270:19269-19276, 1995). pGL3-Basic and pGL3-Control (Promega, Madison, WI) were used as transfection controls for comparison across the cell lines. Relative expression of the pGL3-OB plasmids in pre-adipocytes was several fold lower than the primary adipocytes (raw luciferase values of ~5,000 vs. ~25,000 in a comparable assay) and the data are presented as relative levels within a given cell type.

B. Calcium phosphate transfection

3T3-L1 cells or other cell lines were plated at ~60% confluency and allowed to adhere to the plate overnight. The following day calcium phosphate DNA precipitates containing 2 µg of pGL3B-OB1 DNA were prepared and added to the cells for 8 hours. The cells were washed and refed with media containing 10% FBS and 200 µM insulin. After 48 hours the cells were washed and lysed for luciferase measurements using standard commercial reagents and protocols (Promega).

C. Assaying for tissue specific promoter activity

The expression of the *ob* mRNA is specific for adipose tissue and strongly regulated in rodents (Frederich, et al., (1995) J. Clin. Invest 96:1658-1663; MacDougald, et al., (1995) Proc. Nat. Acad. Sci. USA 92:9034-9037; Saladin, et al., (1995) Nature 377:527-529; Trayhurn, et al., (1995) FEBS Lett. 368:488-490; DeVos, et al., (1995) J. Biol. Chem 270:15958-15961; Murakami, et al., (1995) Biochem. Biophys. Res. Commun. 214:1260-1267).

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(-220)

(-220)

5

KpnI

XhoI

GGGGCGGGGCGGGAGCTGCGCTAGAAATGCGCCGGGGCCTGCGGGGCAGTTGCGCAAGTTGT

10

SP1

C/EBP

15

GCAGCGCCAA CGGTTGCAAG (+30)

An AT-rich sequence 31 bp upstream of the transcription initiation site, TATAAGA, resembles a TATA box. The sequence immediately upstream of the transcription initiation site is extremely GC-rich, including several consensus Sp1 binding sites, implicating Sp1 in the expression of this gene. A C/EBP protein binding site is located at -45.

There are potential binding sites for the insulin responsive ETS family members SAP-1 and ELK-1 further upstream from the proximal promoter. Consensus sites containing CGGA or its complement TCCG are set in bold face and underlined in SEQ. ID NO. 4 (Jacob, et al. J. Biol. Chem. 270:27773-27779, 1995). CTTCGG, TCTCCG, and TCCGCGGA as indicated in SEQ ID NO.4 are likely to mediate insulin response of this ob promoter. Similar sites have been found in the insulin responsive genes somatostatin, thymidine kinase and prolactin, and several other genes which are regulated at the

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transcriptional level by insulin including phosphoenolpyruvate carboxykinase, glyceraldehyde 3-phosphate dehydrogenase and growth hormone. Id.

pGL3-OB1 was transfected into primary rat adipocytes, mouse 3T3-L1, CV-1 and COS cells. Figure 17 (B) shows the basal level of the human *ob* gene promoter activity in 3T3-L1 cells as compared to the control plasmid (pGL3-Basic) with no *ob* promoter. Figure 17 (B) also shows that the *ob* promoter enhanced luciferase expression two-fold in response to insulin whereas the control was unaffected.

Relative to the promoterless parent vector the human *ob* promoter fragment stimulated luciferase expression up to 15-fold in primary rat adipocytes (Figure 18). In the 3T3-L1 cells maintained under non-differentiating conditions, luciferase expression was 10- to 15-fold higher in the pGL3-OB1 transfected cells relative to the pGL3-Basic vector. In CV-1 cells, the same *ob* promoter fragment induced luciferase expression by < 2.5-fold. Similar results were obtained with COS cells. These results are consistent with the observation that *ob* mRNA expression is primarily observed in adipocytes and preadipocytes. The results show that the sequences necessary for adipocyte lineage specific expression of the *ob* gene are contained within the 3 kb HindIII fragment in pGL3-OB1 and suggest the existence of tissue-specific regulatory elements.

To further define areas within this 3 kb region that are important for *ob* gene expression in adipocytes, pGL3-OB2 was used to transfect primary rat adipocytes, 3T3-L1 and CV-1 cells. pGL3-OB2 had comparable promoter activity to pGL3-OB1 in adipocytes, while the expression in non-adipocyte lineages

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remained low (Figure 18C). The difference in expression level between adipocytes and cells from different origins suggests the existence of the region necessary for basal expression of ob gene and tissue-specific regulatory elements localized to the proximal 217 bp as evidenced by the robust expression of pGL3-OB2.

D. Delineating other control regions

C/EBP α site

Adipocyte differentiation has been shown to be determined by the coordinately acting transcription factors PPAR γ (Freytag, S.O. & Geddes, T.J. (1992) *Science* 256:379-382) and various members of the C/EBP family (Schoonjans, et al., (1995) *J. Biol. Chem.* 270:19269-19276; Freytag, S.O. & Geddes, T.J. (1992) *Science* 256:379-382; Freytag, et al., (1994) *Genes and Development* 8:1654-1663) among others. Since we had identified a potential binding site for C/EBP in the promoter, we examined its role in the expression of the ob gene. Co-transfection of C/EBP with pGL3-OB1 or pGL3-OB2 in rat primary adipocytes as well as in 3T3-L1 preadipocytes induced ob promoter activity significantly (Figure 19A & B). In primary rat adipocytes, expression of both the 3kb promoter construct, pGL3-OB1, and the 217 bp construct, pGL3-OB2, were stimulated 2.5 to 4-fold. In 3T3-L1 cells, C/EBP α cotransfection stimulated the expression of the two reporter vectors pGL3-OB1 and pGL3-OB2 by about 2.5 fold. No significant effect was seen on the promoterless control.

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The expression of the pGL3-OB1 reporter vector was furthermore induced in a concentration-dependent way by C/EBP α in rat primary adipocytes (Figure 19C). The fact that the stimulation was seen with both the pGL3-OB1 and pGL3-OB2 constructs indicates that the sequence identified by computer search and contained within the 217 bps adjacent to the transcription initiation site was responsible for the increased luciferase expression.

To further test this hypothesis, we mutated the consensus C/EBP site at nucleotide positions -53 to -45 from TTGCGCAAG to TTAAAAAAG (mutant nucleotides underlined) in the pGL3-OB1 vector. When the mutant C/EBP construct pGL3-KOB1 was introduced into primary rat hepatocytes, basal luciferase expression was reduced by more than 30% and the 2-fold stimulation of the wild-type promoter construct seen upon co-transfection with C/EBP α was absent, demonstrating that in the 3 kb promoter, this site was functional in mediating the effect of C/EBP α on *ob* gene expression.

The function of the Sp1 binding site can be analyzed using the same approach. Sp1 protein and its binding site are co-factors for basal and regulated transcription for genes such as the LDL receptor. The Sp1 binding site may be another positive transcription element for the *ob* gene promoter. In that regard, a Sp1 agonist would be an up regulator whereas a Sp1 antagonist would be a down regulator for the *ob* gene expression.

Negative regulators

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Deletion constructs are useful for identifying and dissecting the control regions of the 5' promoter sequences. So are internal deletions and scrambled mutations for characterizing individual factor binding sites as demonstrated above for the C/EBP site. Nested deletions of the pGL3-OB1 construct were made as follows: The pGL3-OB1 vector was digested with SacI and MluI and treated with exonuclease III and S1 nuclease as described (Henkoff, *Gene* 28:351-359, 1984). The DNAs were treated with Klenow, ligated overnight at 20°C, and used to transform E. coli XL1-Blue cells. Positive clones were analyzed by restriction digestion and dideoxy-sequencing.

The deletion constructs that were selected for further experiments were pGL3-OBA5, containing sequences from -1869 to +31, and pGL3-OBA12, which contained sequence from -978 to +31, both relative to the transcription initiation site. The hamster expression vector pSG5-cgPPAR γ was described elsewhere (Aperlo, et al., *Gene* 162:297-302, 1995).

pGL3-OB1, pGL3-OB2, pGL3-OBA5, pGL3-OBA12, and control plasmid without ob gene promoter were transfected into 3T3-L1 cells together with pSG5 or pSG5-cgPPAR γ . The presence of PPAR γ consistently downregulates the expression from the human ob gene promoter as was demonstrated for the endogenous gene expression in animals and cultured rat adipocytes treated with PPAR γ agonists.

As shown in Figure 25, deleting sequences localized upstream of -1869 or -978 from the transcription initiation site increased the level of expression of the ob promoter. This suggests the presence of negative transcription elements suppressing the ob gene transcription in the regions from -217 to -978 and to -1869. Since interference with the function of

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these negative transcription elements would allow a higher level of *ob* gene expression and augmenting the activity of these negative transcription elements would reduce the level of *ob* gene expression, this invention envisions screening for modulators of these negative transcription elements and using deletions and mutations to further isolate control regions from -217 to -1869.

The following clones are tested for transcription activity: pGL3-OB4 (-170 to +31), pGL3-OBΔ8 (-2411 to +31), pGL3-OBΔ14 (-1716 to +31), and pGL3-OBΔ2 (-2382 to +31).

II. Screening for Modulators of *ob* Gene Expression

Cloning of the control regions of the *ob* gene provides a powerful tool for dissecting the role of the *ob* gene product in obesity and other metabolic disorders, including diabetes, cardiovascular disease, cachexia and anorexia. It also provides novel tools for discovering pharmacologic modulators of *ob* gene expression.

The utility of such genetic control elements is far-ranging, extending from their use as tissue specific promoters to drive heterologous gene expression to the fine-tuning of metabolic processes involved in energy, carbohydrate and fat metabolism. The identification and characterization of the promoter, enhancer and silencer regions of the *ob* gene allows us to identify and understand the discreet control elements involved in the control of the *ob* promoter, likely including among others glucocorticoid response elements (GRE), peroxisome proliferator response elements (PPRE), thyroid hormone response elements (TRE), retinoic acid response elements (RARE), retinoid X response elements (RXRE), estrogen

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response elements (ERE), progesterone response elements (PRE), androgen response elements (ARE), insulin receptor response elements, as well as transcription regulatory binding sites for the helix-loop-helix family members sterol regulatory element binding protein family (SREBP) or its adipocyte expressed homologue ADD-1, CAAT/enhancer binding protein (C/EBP), AP-1, and growth hormone (GH). Such elements are important for the development of screening assays for modulators of *ob* gene expression .

Therefore, a primary utility of the present invention is to provide a model system in which to study the effects of candidate compounds of the classes described herein and by reference, acting upon the transcription factor classes described herein among others and general transcription machinery of the cell to modulate the transcription, either negatively or positively, of the *ob* gene itself or of a reporter gene subcloned in place of the coding sequence of the *ob* gene.

Assay systems using cells

The host cells used in the screening assay herein generally are mammalian cells, and preferably are human cell lines.

Mammalian cells of choice are preadipocyte or adipocyte, e.g., 3T3-L1 or 3T3 F422A or *ob* 1771 (uninduced or induced to differentiate). In a preferred embodiment, isolated rat primary adipocytes are used as a model assay system to screen for *ob* gene modulators.

Isolated adipose cells are among the most responsive cells with respect to glucose transport and metabolism. They

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represent an ideal model to demonstrate insulin sensitivity. (BBRC 1993. 194: 338-346). We used these cells as an assay system to observe the regulation of endogenous *ob* gene expression. These cells, whether derived from rodent, human
5 or other mammalian species, can be used to monitor the expression of a reporter gene driven by *ob* gene control elements or regions.

Inguinal or epididymal fat pads from young rats are removed. Adipocytes are prepared by collagenase digestion
10 (Rodbell, M. J. Biol. Chem. 239:375-380, 1964; and Karneli, E. et al. J. Biol. Chem. 256:4772-4777, 1981). Briefly, cells are washed and resuspended in DMEM at a cytocrit of approximately 40%.

Plasmid DNA containing the control regions of the *ob*
15 gene operatively linked to a reporter gene is introduced into the adipose cells via electroporation technology (Quon, M.J. et al. BBRC 194: 338-346, 1993).

Rat primary adipocytes were isolated and incubated in the presence of (a) insulin (100 nM), (b) dexamethasone (33
20 nM) (c) insulin and dexamethasone, or (d) without the presence of insulin or dexamethasone. After 48 hours of incubation total adipocyte RNA was prepared. 10 μ g RNA per lane was electrophoresed on a gel and blotted to filters and probed with labeled mouse cDNA encoding the *ob* gene. Filters were
25 washed and exposed to films.

The Northern blot showed that both dexamethasone and insulin stimulated production of the *ob* messenger RNA, and their stimulation effects were additive. Dexamethasone provided stronger stimulation of *ob* gene expression than
30 insulin. Therefore, the rat primary adipocytes provide an

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assay system to evaluate the regulation and modulation of *ob* gene expression and a screen for *ob* gene modulators.

Other cell lines may also be used, for example, HeLa, CV-1, HepG2, 293, Hlg 82, MCF-7, CHO, COS-1 through COS-7, HS578T, VERO, W138, BHK, and MDCK either transiently or more preferably stably transfected or otherwise expressing such reporter constructs provided that the *ob* gene control sequence used in such a heterologous system influences transcription from the heterologous gene.

Cell systems other than mammalian may also be used in the screening assays, such as *Drosophila* (SL-2, Kc or others) and yeast strains (permeabilized or not) such as *S. cerevisiae* or *S. pombe* provided that factors necessary for the adipocyte specific expression pattern can be incorporated.

Reporter sequences

Generally, reporter genes encode a polypeptide not otherwise produced by the host cell which is detectable by in situ analysis of the cell culture, e.g., by the direct fluorometric, radioisotopic or spectrophotometric analysis of the cell culture without the need to remove the cells for signal analysis from the culture chamber in which they are contained. Preferably the gene encodes an enzyme which produces colorimetric or fluorometric changes in the host cell which is detectable by in situ analysis and which is a quantitative or semi-quantitative function of transcriptional activation. Exemplary enzymes include luciferase, chloramphenicol acetyl transferase, β -galactosidase, secreted placental alkaline phosphatase, human growth hormone, esterases, phosphatases, proteases (tissue plasminogen

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activator or urokinase) and other secreted enzyme reporters and other enzymes whose function can be detected by appropriate chromogenic or fluorogenic substrates known to those skilled in the art.

- 5 A preferred example is *E. coli* β -galactosidase. This enzyme produces a color change upon cleavage of the indigogenic substrate indolyl-B-D-galactoside by cells bearing beta-galactosidase (see, e.g., Goring et al., Science 235:456-458 (1987) and Price et al., Proc. Natl. Acad. Sci. 10 USA 84:156-160 (1987)). Thus this enzyme facilitates automatic plate reader analysis of ob control region mediated expression directly in microtiter wells containing transformants treated with candidate activators. Also, since the endogenous β -galactosidase activity in mammalian cells 15 ordinarily is quite low, the analytic screening system using β -galactosidase is not hampered by host cell background.

- Another class of reporter genes which confer detectable characteristics on a host cell are those which encode polypeptides, generally enzymes, which render their 20 transformants resistant against toxins, e.g., the neo gene which protects host cells against toxic levels of the antibiotic G418 a gene encoding dihydrifolate reductase, which confers resistance to methotrexate or the chloramphenicol acetyltransferase (CAT) gene (Osborne et al., Cell, 42:203- 25 212 (1985). Resistance to antibiotic or toxin requires days of culture to confirm, or complex assay procedures if other than a biological determination is to be made.

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Other genes for use in the screening assay herein are those capable of transforming hosts to express unique cell surface antigens, e.g., viral env proteins such as HIV gp120 or herpes gD, which are readily detectable by immunoassays.

5 The polypeptide products of the reporter gene are secreted, intracellular or, as noted above, membrane bound polypeptides. If the polypeptide is not ordinarily secreted it is fused to a heterologous signal sequence for processing and secretion. In other circumstances the signal is modified
10 in order to remove sequences that interdict secretion. For example, the herpes gD coat protein has been modified by site directed deletion of its transmembrane binding domain, thereby facilitating its secretion (EP 139,417A). This truncated from of the herpes gD protein is detectable in the culture medium
15 by conventional immunoassays. Preferably, however, the products of the reporter gene are lodged in the intra-cellular or membrane compartments. Then they can be fixed to the culture container, e.g. microtiter wells, in which they are grown, followed by addition of a detectable signal generating
20 substance such as a chromogenic substrate for reporter enzymes.

ob gene control regions

25 In general, an ob gene promoter is employed to control transcription and hence influence expression of the reporter gene. ob gene promoter is optionally combined with more potent promoters, e.g. the TK or SV40 early promoter described in the Examples infra in order to increase the sensitivity of the screening assay.

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A preferred condition would be to use the sequences upstream or 5' to the transcription initiation site or the coding sequence as the control elements, with or without additional promoter elements such as a TATA sequence or other sequences as may be required and obvious to one practiced in the art of heterologous gene expression and with or without intron sequences fused to a reporter gene to measure the effects of candidate compounds added to the cell culture.

The = 3 kb human genomic sequence upstream of the 5' exon in Figure 9 is amplified by PCR with SMREV and the M13 - 20 primers using the HindIII subclone in pBSII-SK+ as a template and ligated immediately upstream to the start codon of the reporter gene with or without additional control elements. The recombinant DNA so constructed is used to regulate the expression of a reporter gene in a cell line.

The *ob* gene promoter, whether a hybrid or the native *ob* gene promoter, is ligated to DNA encoding the reporter gene by conventional methods. The *ob* gene promoter is obtained by in vitro synthesis or recovered from genomic DNA. It is ligated into proper orientation (5' to 3') adjacent 5' to the start codon of the reporter gene with or without additional control elements. The region 3' to the coding sequence for the reporter gene will contain a transcription termination and polyadenylation site, for example the hepatitis B or SV40 polyA site. The promoter and reporter gene are inserted into a replicable vector and transfected into a cloning host such as *E. coli*, the host cultured and the replicated vector recovered in order to prepare sufficient quantities of the construction for later transfection into suitable eukaryotic host.

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The screening assay typically is conducted by growing the *ob* gene promoter transformants (e.g. stably transformed) to a suitable state of confluency in microtiter wells, adding the candidate compounds to a series of wells, and determining the signal level after an incubation period that is sufficient to demonstrate a measurable signal in the assay system chosen. The wells containing varying proportions of candidates are then evaluated for signal activation. Candidates that demonstrate dose related enhancement of reporter gene transcriptions or expression are then selected for further evaluation as clinical therapeutic agents. Candidate compounds may be useful therapeutic agents that would modulate *ob* gene expression.

The *ob* gene control region, including, but not limited to, that included in the P1 clones (5135, 5136 and 5137) deposited at ATCC may be introduced into animals by transgenic techniques, such as those disclosed in PCT publication WO 94/18959, incorporated by reference herein.

Transgenic mice carrying the P1 clones described herein which contain the human *ob* gene locus of approximately 85 kilo bases with regulatory flanking sequences can be used both as a primary screening vehicle in which compounds can be administered and parameters such as feeding, weight and *ob* mRNA production can be measured along with other appropriate controls to effectively assess the changes in expression of *ob* mRNA as well as a means of corroborating primary compound positives.

Alternatively, the P1 clone DNA carrying the *ob* gene locus could be introduced into animals utilizing adenovirus drag technology in which the target DNA is admixed

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with poly-L-lysine and/or transferrin or asialoglycoprotein modified adenovirus and injected i.v. into the animal, resulting in expression of the foreign DNA (Wu et al., JBC 266:14338-14342, 1991; Yanow et al. 1993, PNAS 90:2122-2126).

- 5 In a preferred embodiment, recombinant adenovirus carrying the exogenous DNA can be injected directly into fat deposits of mice, rats or other species as has been done previously in brain (Davidson, Nature Genetics 3:219, Science 259:988) , muscle (Quantin, PNAS 89:2581) (Statford-Perricaudet J. Clin. Invest. 90:626), and tumors. These animal model assay systems are also useful in secondary characterization and study of compounds found to regulate *ob* gene expression identified in other assays.

- 15 Additionally, the coding region of the *ob* gene in this P1 clone construct can be replaced with a reporter gene as described above which could be then introduced into animals either via the standard transgenic practice or through the use of adenoviral drag or other methods of introducing foreign DNA into animals.

20

Example 1: Assaying for modulators of *ob* gene expression

- Since the *ob* gene is exclusively expressed in adipocytes, adipogenic factors likely play major roles in the expression and regulation of the *ob* gene. The expression of two important adipocyte transcription factors, PPAR γ and C/EBP α , is induced during adipocyte differentiation and these factors are maintained in the mature adipocyte. Several adipocyte-specific genes have binding sites for these factors in their promoters and have been shown to be transcriptionally responsive to chemical modulators of these factors. The
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effect of C/EBP α on ob gene expression mediated by a C/EBP site in the proximal ob gene promoter has been shown in this application.

5 The effects of antidiabetic thiazolidinediones (TZDs), previously shown to be ligands for PPAR γ (Lehmann et al., Journal of Biological Chemistry 270:12953-956, 1995, not admitted to be prior art), on expression of the ob gene were examined *in vivo*, *ex vivo* in primary adipocyte cultures, and *in vitro* in transfected cells.

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In vivo assay in rats

To test the effects of drugs, rats were dosed once per day by oral gavage with vehicle alone or containing 1, 2 or 5 mg/kg body weight for seven days. At the end of the dosing period, the rats were sacrificed and tissues collected for mRNA analysis. Fat was collected for ob mRNA analysis and RNA samples were prepared from each individual animal (4 per group). Northern blot analysis was performed normalizing the ob mRNA signal to an actin signal as an RNA loading control.

20 The effects of the antidiabetic thiazolidinedione BRL 49653 on the expression of the ob gene was tested *in vivo* in rats. In animals receiving BRL 49653 at increasing doses (0, 1, 2, and 5 mg/kg/day) over 7 days no change in either body or liver weight was observed (Table 5). The absence of an effect on total body weight is likely due to the short time of treatment.

25 A dose-dependent increase in epididymal fat pad weight was observed after BRL 49653 treatment (Table 5). The ratio of adipose tissue/body weight increased significantly (0.75% \pm 0.1 before vs. 1.2% \pm 0.2 after treatment; $p < 0.05$) in

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animals treated with BRL-49653 (5 mg/kg/day), indicating that some remodeling of the body fat was occurring. BRL 49653 may contribute to fat redistribution in humans as well. Since the modulation of *ob* gene expression may be a part of the fat redistribution process, visceral fat increases associated with the metabolic syndrome or syndrome X may be controlled (e.g. increased or decreased) by *ob* gene modulators.

In this experiment, which used relatively low doses of BRL, food intake showed a tendency to decrease, although no statistical significance was obtained. When higher doses of BRL 49653 (5, 10, 20 mg/kg/day) were administered to rats over 7 days, a significant dose dependent increase in food intake was observed (Figure 22).

ob mRNA levels in epididymal fat pads of these rats decreased by 40% in rats treated with BRL 49653 (5 mg/kg/day) (Figure 20). The effect of BRL 49653 on *ob* mRNA expression was furthermore dose-dependent (Figure 23).

Other potential conditions resulting in activation of PPAR γ , such as administration of a diet enriched in fish oils (20% w/w in food, 3 months), also decreased *ob* mRNA expression significantly by 33% (Figure 2). Therefore, fatty acid-derived PPAR activators are modulators of *ob* gene expression.

In contrast to the results obtained with thiazolidinediones and fish oils, administration of the PPAR α activator, fenofibrate (0.5% w/w in food for 14 days), did not result in a reduction of *ob* mRNA levels (Figure 20). Treatment of animals with fenofibrate did not result in a change in body or adipose tissue weight, whereas the typical increase in liver weight (from 13.8 \pm 0.5 to 19.7 \pm 2.5 g)

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known to occur after treatment with peroxisome proliferators such as fenofibrate, was observed.

Ex vivo assay in primary adipocyte cultures

5 Primary rat adipocytes were obtained exactly as described by Hajduch et al. (1992) *J. Cell. Biochem.* 49:251-258. In order to determine whether the *in vivo* changes in *ob* gene expression are the result of a direct effect on adipocyte *ob* gene expression, the effects of BRL 49653 (100
10 μ M; 24 hr) and the peroxisome proliferator, fenofibric acid (250 μ M; 24hr), on *ob* mRNA expression were evaluated in primary rat adipocytes. Whereas BRL 49653 reduced *ob* mRNA expression significantly in three independent experiments, no effect of fenofibrate on *ob* mRNA levels was detected (Figure
15 21A). These data confirm that the *in vivo* effects of the PPAR activators are due to a direct cellular effect on adipocyte *ob* gene expression.

In vitro in transfected cells

20 The effects of co-expression of PPAR γ in the presence or absence of PPAR agonists on the human *ob* promoter construct pGL3-OB1 were examined.

In primary rat adipocytes, cotransfection of hamster PPAR γ expression vector (pSG5-cgPPAR γ) had minimal effect on
25 basal activity observed in the absence of ligands or activators (Figure 21B). Pioglitazone (PIO, 10 μ M) alone gave about 30% decrease in pGL3-OB1 expression, which further decreased to about 50% inhibition when PPAR γ was cotransfected (Figure 21B). When a more potent thiazolidinedione, such as
30 BRL 49653 (10 μ M), was used in rat primary adipocytes, the *ob*

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promoter activity was reduced to 40% and cotransfection of PPAR γ had no further effect, suggesting the presence of saturating amounts of endogenous PPAR γ in the mature adipocyte (Figure 21B).

5 Treatment of the undifferentiated 3T3-L1 preadipocytes with thiazolidinediones by themselves had no effect on *ob* promoter activity in pGL3-OB1 because these cells, unlike primary adipocytes, do not contain PPAR γ (Tontonoz, et al. (1994) *Cell* 79:1147-1156). Cotransfection
10 of PPAR γ in undifferentiated 3T3-L1 cells, however, reduced the activity of the pGL3-OB1 promoter construct. The degree of inhibition was dependent on the amount of PPAR γ cotransfected. The addition of BRL 49653 had a slight cumulative effect.

15 In summary, the administration of the thiazolidinedione BRL49653, a PPAR γ ligand, increased food intake and adipose tissue weight in rats while reducing *ob* mRNA levels in a dose-dependent manner. The inhibitory action of BRL49653 on *ob* mRNA levels was also observed *in vitro*.
20 Thiazolidinediones (also including pioglitazone) reduced the expression of the human *ob* promoter in primary adipocytes. However, in undifferentiated 3T3-L1 preadipocytes lacking endogenous PPAR γ , cotransfection of PPAR γ was required to observe the decrease in *ob* mRNA. These data suggest that
25 PPAR γ activators reduce *ob* mRNA levels through an effect of PPAR γ on the *ob* promoter.

 The above assays have screened out PPAR γ agonists, thiazolidinediones, BRL49653 and pioglitazone as modulators of an *ob* gene control region.

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Other candidate compounds

The following compounds can be screened by the assays described and disclosed in this application for modulators of an ob gene control region:

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1. Glucocorticoid Receptors

Compounds disclosed in Spiegelman et al., *J. Biol. Chem.* 264:1811-1815, (1989), Muglia et al., *Nature* 373:427-432, (1995) and Williams et al., *Mol. Endocrinol.* 5:615-618 (1991) are incorporated by reference herein.

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2. Thyroid Hormone Receptors (T₃R family)

Thyroid hormones are known to have important effects on body weight homeostasis. On the one hand, in hyperthyroidism an increase in food intake has been observed, whereas in hypothyroidism food intake decreases significantly. Thyroid hormone is not only known to affect food intake but is also known to regulate basal metabolic rate (see chapters 9, 10, and 17 of Cryer et al., *New Perspectives in adipose tissue: structure, function and development*, London: Butterworths p. 474 (1985)) and adipose differentiation (Gharbi-Chibi et al., *Biochim. Biophys. Acta*, 1177:8014 (1993)). Due to this effect on basal metabolic rate one sees often a dissociation of the effects on body weight and food intake, suggesting that the effect on basal metabolic rate is the predominant one.

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This was confirmed in a study analyzing the effects of thyroid hormone on body weight and food intake (Staels et al., *Endocrinology* 127:1144-1152 (1990)). Administration of thyroxine to make rats decrease in body weight despite an

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increase in food intake. Reduction of thyroid hormone levels by the administration of N-propyl-thiouracil results in a significant increase in body weight despite the fact that the animals ingest less food. These data show that thyroid function has a major impact on body weight. Therefore thyromimetics might be useful drugs for the treatment of obesity. Compounds disclosed in Underwood et al. Nature 324:425-429, 1986 are incorporated by reference herein. The thyromimetics disclosed in a European Patent Application entitled "Oxamic acid derivatives as hypocholesteremic agents" (Application Number 93810495.7, publication NO. 0580550A1, January 26, 1994) are also incorporated by reference herein.

3. Peroxisome Proliferator Activated Receptors and their Agonists and Antagonists

In contrast to the development of brown adipose tissue (BAT), which takes place mainly before birth, the development of WAT is the result of a continuous differentiation/development process throughout life (Lardy et al., *Annu. Rev. Biochem.* 59:689-710 (1990), Spiegelman et al., *J. Biol. Chem.* 268:6823-6826 (1993) and Aihauld et al., *TEM* 5:132-135 (1994)). During development, cells that are pluripotent become increasingly restricted to specific differentiation pathways. This process which culminates with differentiation into adult tissues undoubtedly involves a coordinate sequence of changes in gene expression reflected by the synthesis of increasingly specialized proteins.

Adipocyte differentiation from adipose precursor cells, or adipoblasts, has been shown to be orchestrated by two interdependently acting transcription factors: PPAR γ

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(Tontonez et al., *Genes & Development* 8:1224-1234 (1994) and Tontonez et al., *Cell* 79:1147-1156 (1994)) and CCAATT enhancer binding protein α (C/EBP) (Christy et al., *Genes & Development* 3:1323-1335 (1989), Freytag et al., *Science* 256:379-382, 5 (1992) and Freytag et al., *Genes & Development* 8:1654-1663 (1994)). Although both factors are capable of inducing terminal adipocyte differentiation, current evidence favors PPAR γ as the initial trigger (Tontonez et al., *Cell* 79:1147-1156 (1994)).

10 In fact, expression of PPAR γ occurs earlier than expression of C/EBP α during adipocyte differentiation. Furthermore, in contrast to C/EBP α , a transcription factor occurring in multiple tissues, PPAR γ shows an adipose-restricted pattern of expression. Therefore the currently 15 favored hypothesis suggests that PPAR γ provides the initial trigger for the adipogenic program, whereas the terminal differentiation would require the concerted action of both PPAR γ and C/EBP α .

At present 4 distinct peroxisome proliferator 20 activated receptors (PPAR) have been described, i.e. α , β , γ , δ (Dreyer et al., *Cell* 68:879-887, (1992) and Kliewer et al., *Proc. Natl. Acad. Sci. USA*, 91:7355-7359 (1994)). PPARs are members of the superfamily of nuclear hormone receptors, which after ligand activation, regulate the expression of genes 25 containing a specific response elements, called PPRES in their regulatory sequences (Osumi et al., *Biochem. Biophys. Res. Commun.* 175:866-871 (1991) and Tugwood et al., *EMBO J.* 11:433-439 (1992)). Functional PPRES have been characterized in several genes involved in the control of lipid metabolism 30 (Osumi et al., *Biochem. Biophys. Res. Commun.* 175:866-871

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(1991), Tugwood et al., *EMBO J.* 11:433-439 (1992), Zhang et al., *Proc. Natl. Acad. Sci. USA* 89:7541-7545 (1992), Marcus et al., *Proc. Natl. Acad. Sci. USA* 90:5723-5727 (1993), Alvarez et al., *Canc. Res.* 54:2303-2306 (1994), Bardot et al.,
5 *Biochem. Biophys. Res. Commun.* 192:37-45 (1993) and Tontonez et al., *Cell* 79:1147-1156 (1994)).

The transcriptional activity of the PPARs can be induced by various peroxisome proliferators (such as hypolipidemic fibrate drugs, plasticizers such as di-(2-
10 ethylhexyl)-phtalate, or herbicides such as 2,4,5-trichlorophenoxyacetic acid) as well as by long chain fatty acids (Auwerx, *J. Hormone Research* 38:269-277 (1993)). This panoply of potential stimulators supports the current hypothesis that endogenous fatty acids are the true ligands
15 for PPAR.

Whereas the endogenous ligands and activators of PPAR activity most likely are fatty acids, it is even more striking that most of the above mentioned PPAR target genes control various aspects in lipid metabolism. This points to a
20 pivotal role of PPAR in the control of lipid metabolism and suggests that this factor might function as the key signaling molecule in many lipid and nutritionally controlled signalling pathways.

Coherent with this important role of PPAR in
25 controlling lipid metabolism was the recent demonstration that one of the PPAR isoforms, PPAR γ , was the key transcription factor triggering adipocyte differentiation (Tontonez et al., *Cell* 79:1147-1156 (1994)), and as such is involved in the direct transcriptional switch-on of several marker genes for
30 adipocyte differentiation, including lipoprotein lipase and

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aP2 (Tontonez et. *Genes & Development* 8:1224-1234 (1994) and Tontonez et al., *Cell* 79:1147-1156 (1994)). The administration of PPAR γ agonists resulted in a marked reduction of adipose tissue *ob* mRNA levels.

- 5 Genes with functional PPRES have been identified both in the LPL and the aP2 (Tontonez et al., *Genes & Development* 8:1224-1234 (1994) and Tontonez et al., *Cell*, 79:1147-1156 (1994)). This suggest that this nuclear hormone receptor is involved in differentiation pathways, a hypothesis supported
10 by our recent studies on the lipoprotein lipase gene expression in the liver. The expression of LPL in the liver has been shown to be extinguished after birth, in a process very closely resembling the extinction of α -fetoprotein (Staels et al., *Development* 115:1035-1043 (1992)).
15 Interestingly, administration of fibric acid derivatives or FFAs can reinduce the expression of LPL in the liver (Staels et al., *Development* 115:1035-1043 ((1992)), suggesting that the development role of PPAR is not limited to adipocytes.

- Without being bound by any theory, Applicant
20 proposes that *ob* gene may be silenced in tissues other than white fat cells. The silenced *ob* gene in a non-WAT cell may be turned on by an *ob* gene modulator to provide therapeutic effects.

- FFA plays a role in adipose differentiation
25 (Tontonez et al, 1994, *Genes & Development* 8:1224-1234, Tontonez et al., 1994, *Cell* 79:1147-1156, Amri et al., 1991, *J. Lipid Res.* 32:1449-1456 Amri et al., 1991, *J. Lipid Res.* 32:1457-1463, Chawla et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:1786-1790 and Grimaldi, 1992, *Proc. Natl. Acad. Sci. USA*
30 89:10930-10934).

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Fatty acids (Tontonoz, et al., (1994) Cell 79:1147-1156; Amri, et al., (1991) J. Lipid Res. 32:1449-1456; Chawla, A., and M.A. Lazar (1994) Proc. Natl. Acad. Sci. USA 91:1786-1790), arachidonic acid (Gaillard, et al., (1989) Biochem. J. 257:389-397), antidiabetic thiazolidinediones (Lehmann, et al., (1995) J. Biol. Chem. 270:12953-12956; Forman, et al., (1995) Cell 83:803-812), prostaglandin derivatives (Forman, et al., (1995) Cell 83:803-812; Kliewer, et al., (1995) Cell 83:813-819), and compounds disclosed in Tontonez et al., Genes & Develop. 8:1224-1234 (1994), Amri et al., J. Lipid Res. 32:1457-1463, and Grimaldi et al., Proc. Natl. Acad. Sci. USA 89:10930-10934 (1992) are incorporated by reference herein.

In addition to PPAR γ , other PPAR subtypes such as PPAR β (also called FAAR, NUC1, or PPAR δ) and PPAR α play roles in adipocyte differentiation.

PPAR β is expressed in preadipocyte at an earlier stage than PPAR γ , suggesting that it has function in adipocyte differentiation. Agonists and antagonists of PPAR β or agents affecting the expression of PPAR β may have effects on ob gene expression.

Mice deficient in PPAR α (e.g. generated by homologous recombination) develop a pronounced obesity as they age. PPAR α agonist are therefore potential agents decreasing adipocytogenesis and reducing obesity whereas PPAR α antagonists are potential agents increasing adipocyte differentiation and increasing appetite, food intake, body fat content, or body weight.

Agonists and antagonists of PPAR β and PPAR α are candidate compounds for the assays of this invention and modulation of ob gene expression.

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4. Retinoic Acid Receptors and Retinoid X Receptors (RAR and RXR families)

Retinoic acid is known to inhibit adipogenesis in 3T3-F442A and ob 17 cells. Compounds disclosed in Antras et al., *J. Biol. Chem.* 266:1157-1161 (1991), Salazar-Olivo et al., *Biochem. Biophys. Res. Commun.* 204:157-263 (1994) and Safanova, *Mol. Cell. Endocrin.* 104:201-211 (1994) are incorporated by reference herein.

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5. Estrogen Receptors (ER family)

Estrogens are known to have important effects on body weight and food intake. An experiment performed on female rats was published by Staels et al., *J. Lipid Res.* 30:1137-1145 (1989). Both ovariectomy (OVX) and consecutive substitution therapy, with the indicated doses of ethinylestradiol, showed a marked effect on body weight in ovariectomized rats.

This effect was not specific for female rats since changes in body weight and food intake was observed in male mice injected with ethinylestradiol. Whereas sham-injected male mice showed an increase in body weight of $1.81 \pm 1.04\%$, their ethinyl estradiol ($0.75 \mu\text{g/g}$ body weight) injected littermates showed a $14.83 \pm 1.44\%$ decrease in body weight over a 7 day treatment period. The decrease in body weight was associated with an important reduction in food intake.

In order to prove that the decrease in food intake caused by EE was responsible for the change in body weight, we compared body weight between ovariectomized rats and control rats, between ovariectomized rats and ovariectomized rats

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substituted with 20 μ g ethylestradiol (EE) per day, and between ovariectomized rats and ovariectomized rats substituted with 2000 μ g ethinylestradiol per day, who this time had been pair-fed (Staels et al., J. Lipid Res. 30:1137-1145 (1989)). Either the intact animals or the animals which received estrogens were taken as reference in the pair feeding. Interestingly, pair-feeding abolished the effects of estrogens on body weight, suggesting that estrogens exert their effect on body weight by reducing food intake.

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6. Androgen Receptors (AR family)

7. Progesterone Receptors (PR a and b)

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8. Mineralocorticoid Receptors (MR family)

9. Insulin and Insulin Receptors including secretagogue

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10. Helix-Loop-Helix (HLH) transcription factors such as SREBP-like factors and ADD1

The compounds disclosed in Tontonez et al., Mol. Cell. Biol. 13:4753-4759 (1993) are incorporated by reference herein.

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11. CAAT/Enhancer binding proteins (C/EBP)

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C/EBP family members may be responsible for regulating *ob* as adipocytes undergo differentiation. It has been shown that expression of members of the C/EBP family can be modulated by extracellular compounds such as stimulators of the cAMP pathway and glucocorticoids. For example, two lines

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of evidence have shown that C/EBP α is involved in the differentiation of adipocytes. 1) Over expression of C/EBP α induces differentiation. 2) Antisense oligonucleotides to C/EBP α inhibit the differentiation of adipocytes. C/EBP family members have been shown to be regulated in mature adipocytes by insulin. Furthermore, many adipocyte-specific genes involved in differentiation contain C/EBP sites.

12. AP-1 like factors including Protein kinase C and protein kinase A

13. Growth hormones and their agonists and antagonists
Those disclosed in Corin et al., Proc. Natl. Acad. Sci. USA 87:7507-7511 (1990), Uchida et al., Biophys. Res. Commun. 172:357-363 (1990) and Barcellini-Couget et al., Biochem. Biophys. Res. Commun. 199:136-143 (1994) are incorporated by reference herein

14. Tumor necrosis factor (TNF) and related compounds
TNF inhibits the expression of several adipocyte specific genes. This ultimately will result in a loss of differentiated adipose tissue (Kawakami et al., J. Cell. Physiol. 138:1-7 (1989)) and the occurrence of cachexia. It has been recently shown that adipocytes of animals suffering from obesity showed an increased production of TNF (Hotamisligil et al., Science 259:87-91, 1993). The TNF was furthermore linked to the occurrence of insulin-resistance a phenomenon often associated with obesity (Hotamisligil et al., Science 259:87-91 (1993)).

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Without being bound by any theory, it is hypothesized that in normal weight subject TNF is involved in a physiologic feedback loop limiting the development of obesity. In obese animals this feedback process might be
5 disturbed, resulting in a compensatory overproduction of TNF and the development of insulin resistance.

One of the most debilitating effects of cancer and AIDS is the wasting syndrome known as cachexia which often accompanies these conditions. Cachexia is a combination of
10 anorexia, reduced intake of nutrients, and stimulation of catabolic processes leading to protein loss and depletion of lipid reserves. The cytokine tumor necrosis factor (TNF) is often elevated in the plasma of individuals displaying
15 cachexia and was originally termed cachectin as a result of its association with cachexia. Administration of recombinant TNF to animals replicates the effects of cachexia in animals, and administration of anti-TNF antibodies can in some cases
20 alleviate the effects of cachexia.

A target for therapeutic treatment of cachexia would
20 be to block the production of TNF or TNF signal transduction which may play a role in the ob gene expression. The drug pentoxifylline has been tested in cancer patients for the reduction of cachexia and was found to improve the conditions of some patients. Monoclonal antibodies to TNF and soluble
25 TNF (and/or ob gene product mediated) induced cachexia would be of utility in the treatment of wasting associated with chronic conditions such as cancer and AIDS.

Another strategy for therapeutic treatment of cachexia is to down regulate ob gene expression. Without
30 being bound by any theory, applicant proposes that TNF and ob

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gene act synergistically to affect food intake. Inhibitors of TNF and inhibitors of ob production may act synergistically to relieve cachexia.

5 15. Cytokines and growth factors such as IL1 and TGF- β

The compounds disclosed and referred to in Gimble et al., Mol. Cell. Biol. 57:4587-4595 (1989) are incorporated by reference herein.

10 16. Insulin

Insulin levels in blood are increased postprandially, whereas lower insulin levels are found during the interprandial periods. We have preliminary evidence showing that the induction in ob mRNA levels detected after
15 food ingestion in rats relative to fasted animals can be ascribed to higher insulin levels in fed rats. Therefore, insulin administration or elevation of endogenous insulin via the administration of insulin secretagogues could induce ob mRNA levels and increase circulating ob levels. This would be
20 translated into a decrease in food intake.

Candidate compounds include insulin mimetics (Ibrahimi et al., 1994 Mol. Pharmacology 46:1070-1076) and secretagogues, amino acids, free fatty acids, carbohydrates, sulfonamides, biguanides (antidiabetics), metformin,
25 phenformin, pyroglyrides, thiazolidinediones and their antagonists.

17. Adrenergic system

Antagonists might be helpful since adrenergic
30 stimulation promotes preadipocyte proliferation (Bouloumie et

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al., *J. Biol. Chem.* 269:30254-30259 (1994)). In contrast, α -antagonist, phenoxybenzamide, prevents weight gain and fat accumulation. β 3-agonists and antagonists (e.g., ICI compounds D7-114, D2079) which stimulate development of brown adipose tissue are candidate compounds too.

The compounds disclosed and referred to in Lowell et al., *Endocrinology* 126:1514-1520 (1990) are incorporated by reference herein.

10 18. Glucocorticoids, precursors and derivatives (antagonists)

19. Thyroid hormone and thyromimetics

20. Fibrates, antagonists, subtype selective compounds

15 Clofibric acid, fenofibrate, etiofibrate, gemfibrozil and the thiazolidinedione antidiabetic compounds (Ibrahimi et al., *Mol. Pharmacol.* 46:1070-1076 (1994)) are all known to stimulate transcriptional activity of the PPAR nuclear hormone receptors. Inhibitors of PPAR activity are
20 useful as well.

21. PAR-selective agonists and antagonists

The compounds disclosed and referred to in (Antras et al., *J. Biol. Chem.* 266:1157-1161 (1991)) are incorporated
25 by reference herein.

22. RXR-selective agonists and antagonists

23. Estrogens, agonists, partial agonists, partial
30 antagonists and antagonists

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24. Androgens, agonists, partial agonists, partial antagonists and antagonists
25. Progestins, agonists, partial agonists, partial antagonists and antagonists
- 5
26. Mineralocorticoids, agonists, partial agonists, partial antagonists and antagonists
- 10
27. Insulin
28. Fatty acids and sugars
29. Non-steroidal anti-inflammatory drugs (NSAIDs); prostacyclins
- 15
- The compounds disclosed and referred to in Knight et al., *Mol. Endocrinol.* 1:36-43 (1987) and Negrel et al., *Biochem. J.* 257:399-405 (1989) are incorporated by reference herein.
- 20
30. Dihydroepiandrosterone (DHEA), its precursors and derivatives
- DHEA has been known for some time to reduce body weight (for review see Cleary, *Proc. Soc. Exp. Biol. Med.* 196 (1991)). Recently a number of more specific compounds, with a greater effect in reducing body weight and less potential harmful side effects have been developed (Schwartz et al., *Canc. Res.* 48:4817-4822 (1988)). In a short experiment performed in rats, applicant determined that DHEA was capable of reducing the gain in body weight already after a three day
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treatment period. The reduction in body weight was associated with a significant decrease in food intake.

Furthermore, independent on its effects on food intake DHEA has also important effects on adipocyte differentiation (Shantz et al., *Proc. Natl. Acad. Sci. USA* 86:3582-3856 (1989)).

31. TNF, cytokines, and related molecules

10 32. Fetuin

The compounds disclosed and referred to in Gaillard et al., *Biochim. Biophys. Acta* 846:185-191 (1985) are incorporated by reference herein.

15 33. Amylin antagonists and agonists

34. Prolactin

20 35. Niacin, Acepimox and other nicotinic acid derivatives:
These compounds are antilipolytic.

36. Triacsins

The compounds disclosed and referred to in (Tomoda et al., *J. Biol. Chem.* 266:4214-4219 (1991); inhibitors of ACS) are incorporated by reference herein.

37. Amphetamine and derivatives (including fenfluramine and dexfenfluramine)

30 38. Endorphin antagonists

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39. Somatostatin40. Cholecystokinin (CCK)5 41. Bombesin42. Gastrin43. Oral antidiabetic agents and antagonists

10 The compounds disclosed and referred to in Sparks et al., *J. Cell. Physiol.* 146:101-109 (1991) and Hirugan et al., *J. Cell. Physiol.* 134:124-130 (1988) (AD4743) are incorporated by reference herein.

15 Thiazolidinedione antidiabetic compounds (see under fibrates), competitors, agonists, antagonists, homologs, structural analogs thereof and compounds antagonizing thiazolidinedione's action: These compounds strongly activate PPARs. (Ibrahimi et al., *Mol. Pharmacol.* 126:1514-1520 (1990)).

20 The compounds disclosed and referred to in Fong et al., *Biochem. Biophys. Res. Commun.* 181:1385-1391 (1991) (tolbutamide) are incorporated by reference herein.

25 Antidiabetics reviewed by Colca and Morton In New Antidiabetic Drugs; Bailey, C.J., Flatt, P.R., Eds.; Smith-Gordon; 1990 and Stevenson, et al. In Diabetes Annual; Marshall, S., Home, P., Rizza, R., Eds.; Elsevier Science: Amsterdam, 1995; Vol. 9, p 175 are incorporated by reference herein.

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- Exemplary thiazolidinedione candidate compounds include Troglitazone (CS-045) (Yoshioka, et al. J. Med. Chem. 32:421, 1989; Fujiwara, et al. Diabetes 37:1549, 1988); Pioglitazone (AD-4833) (Meguro, et al. U.S. Patent No. 4,687,777, 1987); Ciglitazone (ADD-3878) and analogs (e.g. WAY-120, 744) (Sohda, et al. Chem. Pharm. Bull. 30:3563, 1982; Ellingboe, et al. J. Med. Chem. 36:2485, 1993); BRL 49653 and analogs (Cantello, et al. J. Med. Chem. 27:3977, 1994; Young, et al. Diabetologia 36(Suppl. 1):A75, 1993); Englitazone (Hargrove, et al. In Frontiers in Diabetes Research; E. S., Ed.; Smith-Gordon and Co Ltd: U.K., 1990; Vol. 7, p 313 and references therein); AD 5075 (Williams, et al. Diabetes 42 (Suppl. 1):52A, 1993 and references therein); and Darglitazone (CP-86325) (Hulin, et al. J. Med. Chem. 35:1853, 1992).
- Other related antidiabetic agents to be screened include Oxazolidinediones and oxadiazolidinediones (Dow, et al. J. Med. Chem. 34:1538, 1991; Goldstein, et al. J. Med. Chem. 36:2238, 1993); 5-benzyltetrazoles, (Kees, et al. J. Med. Chem. 35:944, 1992); Hydroxyureas (Goldstein, et al. J. Med. Chem. 36:2238, 1993); and Ciglitazone-like Carboxylic acid derivatives or analogs.

44. CRH

- Hypothalamic administration of corticotropin-releasing hormone into fat rats reduces body weight (Rohner-Jeanrenaud et al., Endocrinology 124:733-739 (1989)). The exact mechanism for this effect is actually unknown. It has been suggested that CRH affects the sympathetic output from the hypothalamus.

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45. Adrenocorticotrophic Hormones, ACTH a and b MSH:

The lethal yellow mutation in mouse, which is associated with an overexpression of the agouti gene product is characterized amongst others by the development of massive obesity and diabetes (Bultman et al., Cell 71:1195-1204 (1992)). It has been shown that the mouse agouti gene interacts with the product of the extension gene (which encodes the melanocyte receptor for alpha-melanocyte stimulating hormone α -MSH) (Lu et al., Nature 371:799-802 (1994)). MSH agonists or antagonists may have an effect on the development of obesity.

46. Gastric inhibitory peptides (GIP)

The compounds disclosed and referred to in Eckel et al., Diabetes 28:1141-1142 (1979) are incorporated by reference herein.

47. Compounds acting through insulin-like growth factor (IGF).III. Treating Diseases with a modulator of ob gene expressionob gene is a target for therapeutic intervention of metabolic disorders and related pathological conditions

White adipose tissue (WAT) is composed of adipocytes, which play a central role in lipid homeostasis and the maintenance of energy balance in vertebrates. These cells store energy in the form of triglycerides during periods of nutritional affluence and release it in the form of free fatty acids (FFA) at times of nutritional deprivation. An excess of

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WAT leads to obesity whereas absence of WAT is associated with lipodystrophic syndromes. In man, obesity is an independent risk factor for several diseases including NIDDM (non-insulin-dependent-diabetes-mellitus), hypertension, infertility and coronary artery disease. An important gene involved in the pathogenesis of obesity is the product of the human homologue of the murine obese gene (i.e., *ob* gene). This gene has been identified by positional cloning in the *ob/ob* mouse (Zhang et al., *Nature* 372:425-432, 1994). The obese mutation in mice is one of five recessive mutations, which give rise to a profound obesity and NIDDM (Friedman et al, *Genomics* 11:1054-1062, 1991), similar to conditions in humans with morbid obesity. Cross-circulation experiments between mutant and wild-type mice suggest that *ob* mice are deficient for a blood-borne factor that regulates nutrient intake and metabolism (Coleman, *Diabetologia* 14:141-148, 1978). This blood-borne factor is considered by some to be identical to the 18 kDa protein synthesized from the *ob* gene.

The *ob* sequence is highly conserved between mouse and man, suggesting an important regulatory function. Its expression is restricted to WAT, suggesting that the *ob* protein, leptin, is a fat-derived satiety factor (Zhang et al., *Nature* 372:425-432, 1994). *ob* mice either have a nonsense mutation resulting in the production of a truncated and non-functional mRNA (C57Bl6J *ob/ob*) or carry a genomic alteration resulting in the absence of mRNA (SM/Ckc-⁺*ob*^{2J}/*ob*^{2J}) (Zhang et al., *Nature* 372:425-432, 1994).

The fact that the *ob* mRNA level in adipose tissue of the C57Bl6J *ob/ob* mice is greatly increased suggests that the level of expression of this gene signals the size of the

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adipose depot. An increase in the *ob* signal (as might occur after prolonged eating) may act directly on the central nervous system (CNS) to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of adipose tissue mass, etc. The level of *ob* expression is inversely correlated with food intake, energy expenditure and the onset of obesity. This invention pertains to using modulators of *ob* gene expression to change the level of *ob* gene expression product (i.e. leptin), which in turn changes the homeostatic status of a host to achieve therapeutic purposes.

Example 2: Reducing body weight gain with
hormones that stimulate *ob* gene expression

15

Applicant studied the effects of high doses of glucocorticoids on the expression of the *ob* gene and changes in body weight and food intake.

Rat was chosen as a model because its body weight and adipose tissue mass keeps increasing throughout its entire life-span, thereby resembling the human situation of adult onset obesity.

Corticosteroids (such as hydrocortisone) are known to exert dual metabolic actions, reflected by a bitonic dose-response curve for body weight gain (Devenport et al. Life Science 45:1389-1396, 1989). In order to evaluate the dose-dependent effects of hydrocortisone on body weight and *ob* gene expression, adult rats were treated once daily during 20 days with 3 different doses of hydrocortisone (1, 10 or 100 μ g/g body weight), resulting in a dose-dependent reduction in body

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weight gain (Figure 4A) accompanied by a dose-dependent induction of *ob* mRNA levels in adipose tissue (Figure 4B).

The results demonstrate that administration of pharmacological doses of glucocorticoids induces adipose tissue *ob* gene expression. This induction is accompanied by reduced food intake and decreased body weight gain in these animals. These data indicate that modification of *ob* gene expression is subject to hormonal/pharmacological regulation, leading to the modulation of caloric intake and body mass gain.

A. Glucocorticoid decreases body weight gain and food intake

80-day-old male rats were treated once daily during 20 days with 100 μ g/g body weight of hydrocortisone. Sham-treated control rats exhibited a significant, steady gain in body weight throughout the treatment period, attaining approximately 110% of the initial body weight after 20 days (Figure 1). Administration of hydrocortisone, however, completely prevented this gain in body weight, and resulted in a slight decrease in body weight at the end of the treatment period (Figure 1).

This difference in body weight gain between control and treated animals became only gradually apparent. During the first 2 days of treatment, body weights did not differ significantly from controls and only thereafter a gradually more pronounced difference was observed.

Compared to untreated animals, hydrocortisone-injected animals consumed 10-15% less food throughout the entire treatment period (Figure 2), indicating that a

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reduction of food intake may, at least in part, account for the lower gain in body weight after hydrocortisone treatment.

B. Glucocorticoid increases ob gene expression in vivo

5 The regulation of adipose tissue ob mRNA expression by hydrocortisone was determined next. Treatment with hydrocortisone increased ob mRNA levels more than 2-fold, and the effect which was maximal after 2 days (Figure 3). ob mRNA levels remained elevated throughout the entire treatment
10 period. This induction was specific because β -actin mRNA levels remained constant throughout the entire treatment period (Figure 3).

 The effects of the synthetic glucocorticoids, dexamethasone and triamcinolone, which are relatively pure
15 type II corticosteroid receptor agonists and produce a more pronounced monotonic negative dose-response curve of body weight gain (Devenport et al. Life Science 45:1389-1396, 1989), were analyzed and compared to hydrocortisone.

 Treatment of adult male rats during 4 days with
20 triamcinolone or dexamethasone also resulted in reduced food consumption (Figure 5A) with concomitant increase of ob mRNA levels (Figure 5B).

 Northern blot hybridization analysis indicated that the ob cDNA probe hybridized to an mRNA of approximately 4.5
25 kb, a size similar to mouse adipose tissue ob mRNA (Zhang et al., Nature 372:425-432, 1994). Furthermore, ob mRNA levels increased 2.2-fold in rat adipose tissue within 24 hr after a single injection of dexamethasone, indicating that the induction of ob gene expression by corticosteroids is a very
30 rapid event.

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These results demonstrate that glucocorticoids induce *ob* expression in rat adipose tissue with concomitant gain in body weight and food intake decrease.

Several lines of evidence support a causal
5 relationship between the induction of *ob* gene expression and a decrease in food intake and body weight.

First, the induction of *ob* gene expression is very rapid and nearly maximal within 24 hr after a single injection of corticosteroids. By contrast, the changes in body weight
10 follow much more gradually, the difference with sham-treated controls only becoming significant after 3 days of treatment. Taking into account that a 16-hour overnight fast reduces the body weight of rats by approximately 7.5% (fed: 376 +/- 12; fasted: 350 +/- 10 grams), it appears that the effects of
15 corticosteroids on body weight changes are much more gradual and lag behind the induction of *ob* gene expression.

Second, the induction of *ob* expression by corticosteroids is independent of food intake, since it is observed regardless whether animals are fed or fasted.

20 Third, it is unlikely that the alterations in *ob* expression are secondary to the decrease in food intake and body weight, since *ob* mRNA levels are increased in hyperphagic C57Bl6J *ob/ob* mice, which have apparently normal regulation of the *ob* gene.

25 Finally, in contrast to normal mice, genetically obese *ob/ob* mice are dramatically resistant to glucocorticoid-induced weight loss (McGinnis et al., *Life Sciences* 40:1561-1570, 1987), indicating that the presence of a functional *ob* gene product is required to transmit the glucocorticoid-
30 induced weight loss.

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Therefore, the induction of *ob* expression after corticosteroid treatment precedes and probably provokes the *ob* gene related alterations in food intake and body weight.

In this respect it is interesting to note that
5 plasma corticosteroid levels are elevated in obese C57B16J *ob/ob* mice (Dubuc, Hormone and Metabolism Research 9:95-97, 1976; Herberg et al., Hormone and Metabolism Research 7:410-415, 1975; and Naeser, Diabetologia 10:449-453, 1974), which may, at least in part, explain the increase in *ob* mRNA levels
10 observed in these mice (Zhang et al., Nature 372:425-432, 1994).

Depending on the dose used, corticosteroids seem to exert a dual metabolic action on gain in body weight and feeding efficiency (Devenport et al. Life Science 45:1389-
15 1396, 1989). Administration of high doses of glucocorticoids, such as in this study, results in a marked decrease in food intake and body weight. In contrast, lower doses of corticosteroids have anabolic activity marked by increased appetite in humans and stimulation of food intake in
20 laboratory animals.

However, in contrast to their catabolic effects, it is unlikely that the anabolic effects of glucocorticoids at low doses are mediated through changes in *ob* gene expression. Indeed, although *ob/ob* mice do not express a functional *ob*
25 gene product, adrenalectomy reduces food intake and normalizes energy balance (Solomon et al., Endocrinology 93:510-513, 1973; Solomon et al., Hormone and Metabolism Research 9:152-156, 1977; and Yukimura et al., Proc. Soc. Exp. Biol. Med. 159:364-367, 1978), whereas corticosteroid replacement therapy
30 restores food intake in these adrenalectomized *ob/ob* mice

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(Saito et al., American Journal of Physiology 246:R20-25, 1984).

The effects of corticosteroids on *ob* gene expression may be due to a direct or indirect action of these hormones on *ob* gene transcription. High doses of glucocorticoids may, for instance, influence the plasma concentrations of other hormones which regulate food intake, such as Dihydroepiandrosterone (DHEA). Glucocorticoids may act by altering plasma concentrations of a modulator of gluconeogenesis, which in turn induces *ob* gene expression resulting in a reduction of food consumption. In this case, factors involved in glucose metabolism, such as glucose itself, glucagon and insulin, would be expected to be important modulators of *ob* gene expression. Low doses (anabolic) of glucocorticoids may produce similar but opposite effects in this metabolic pathway leading to reduced *ob* gene expression and a corresponding increase in food consumption.

Glucocorticoids may also exert their therapeutic effects by binding to a superfamily of intracellular receptors (IRs), which are regulators of gene transcription. The classical mechanism of transcriptional regulation by IRs involves binding of the IRs to specific response elements in the promoters of the regulated genes, for example, the binding of the estrogen receptor to its response site in the vitellogenin gene (Klein-Hitpass et al., *Cell* 46:1053-1061, 1986). More recently a different mechanism of IRs function has been described in glucocorticoid receptor mediated AP-1 transcription regulation that does not require direct DNA-binding of the IRs (Yang-Yen et al., *Cell* 62:1205-1215, 1990).

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Materials and Methods

Animals and treatments

Eighty-day-old male rats received once-daily subcutaneous injections with the indicated corticosteroids at a dose and for the period of time indicated. Control animals received saline only. Rats were group-housed and accustomed to a 12:12 hr day-night illumination cycle. Animals were allowed free access to standard rat chow. Body weight (per animal) and food consumption (per treatment group) were measured at regular intervals throughout the experiment. At the end of the experiment, animals were killed between 9-10 AM by exsanguination while under ether anesthesia. Epididymal fat pads were removed immediately and frozen in liquid N₂.

RNA analysis

Total cellular RNA was prepared by the acid guanidinium thiocyanate/phenolchloroform method (Choeczynski, et al., Analytical Biochemistry 162:156-159, 1987). Northern and dot blot hybridizations of total cellular RNA were performed as described previously (Staels, et al., Development 115:1035-1043, 1992). A mouse ob cDNA fragment spanning nucleotides +50 to +659 was cloned from adipose tissue by reverse transcription and PCR-amplification (sense primer: 5'-CCA AGA AGA GGG ATC CCT GCT CCA GCA GC-3'; antisense primer: 5'CCC TCT ACA TGA TTC TTG GGT ACC TGG CC-3') (Zhang et al., Nature 372:425-432, 1994). a β -actin cDNA clone was used as a control probe (Cleveland, et al., Cell 20:95-105, 1980). All probes were labeled by random primers (Boehringer Mannheim). Filters were hybridized to 1.5×10^6 cpm/ml of each probe as described (Staels, et al., Development 115:1035-1043, 1992).

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They were washed once in 0.5x SSC and 0.1% SDS for 10' at room temperature and twice for 30' at 65°C and subsequently exposed to X-ray film (X-OMAT-AR, Kodak). Autoradiograms were analyzed by quantitative scanning densitometry (Biorad GS670 Densitometer) as described (Staels, et al., Development 115:1035-1043, 1992).

C. Feeding and insulin treatment up regulate ob gene expression in vivo

10 The effects of feeding and insulin on ob gene expression in rats was studied by Applicant. The results demonstrate that in fasting rats the ob gene expression is upregulated by insulin administration or feeding to a similar extent.

15 Adult male Sprague-Dawley rats were group-housed and acclimated to a 12hr:12hr day:night illumination cycle (light from 6 A.M. to 6 P.M.). To determine the diurnal variation of ob gene expression, rats (n=4 per experimental group) were sacrificed at regular intervals (4 hrs) throughout a period of
20 24 hrs.

To study the role of acute food consumption and insulin treatment, rats were divided into 5 groups (n=3 per experimental group). A first group was allowed free access to food and served as a fed control. All other groups were
25 denied access to food during a 12 hr overnight period (the dark cycle). At the beginning of the light cycle, 3 groups of fasted animals received either free access to food, a single injection with insulin (1 U; Actrapid HMge, Novo Nordisk), or both. The last group of fasted animals served as a fasting
30 control. Food consumption was monitored throughout the

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experiment. All animals were sacrificed four hours after insulin administration and/or access to food by exsanguination under ether anesthesia. Epididymal adipose tissue was removed, rinsed with 0.9% NaCl and frozen in liquid nitrogen.

5 RNA isolation, analysis of ob gene expression by Northern hybridization, and quantitation were performed as described above.

As shown in Figure 7, fasted rats that received a single dose of insulin showed about 50-60% increase in adipose
10 tissue ob gene expression relative to fasted rats. Fasted rats that received food showed similar increase relative to the fasted controls.

Since feeding stimulates increases in plasma insulin levels, it was tested to determine if insulin is a mediator of the up regulation of ob gene expression seen in fed animals.
15 As shown in Figure 11, overnight fasting decreased ob mRNA levels to a basal level normalized to 100 relative absorbance units (R.A.U.). A single subcutaneous injection of 1 I.U. insulin resulted in an approximately two-fold increase in ob
20 mRNA 4 hours post injection relative to actin controls as measured by Northern analysis. This is a comparable increase to refeeding after an overnight fast. Refeeding plus insulin gave no additive effects on ob mRNA level. Plasma glucose levels confirmed the effects of administration of insulin and
25 the fed state.

Figure 12 shows the effect of insulin on ob mRNA under hyper- or eu-glycemic clamps. The stimulatory effect of insulin on ob mRNA was maintained when plasma glucose levels were maintained at either high or low levels.

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Insulin also affects ob mRNA expression in primary rat adipocytes. Primary rat adipocytes were cultured in media containing 10% Fetal Bovine Serum (FBS) and treated with either 1 or 10 nM insulin added to the medium. As shown in Figure 13, insulin stimulated the production of ob mRNA in a dose dependent manner.

A similar result is obtained when the ob promoter driven luciferase vector pGL3B-OB1 is introduced into the primary adipocytes. A 140% increase of the level of ob mRNA in media containing 10% FBS is observed upon the addition of 200 nM insulin. Since fetal bovine serum contains insulin which could affect the basal level of expression, the experiment is repeated with a reduced level of FBS to more precisely measure the effects of insulin in this system.

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Example 3: Treating Diseases with a down regulator of an ob Gene

Cachexia is a combination of anorexia, reduced intake of nutrients, and stimulation of catabolic processes leading to protein loss and depletion of lipid reserves.

As shown in Example 1, administration of the thiazolidinedione compound BRL49653, a PPAR γ agonist, increased food intake and adipose tissue weight while reducing ob mRNA levels in rats in a dose-dependent manner. BRL49653 was also observed in vitro to reduce the activity of the human ob promoter in primary adipocytes. In undifferentiated 3T3-L1 preadipocytes lacking endogenous PPAR γ , cotransfection of PPAR γ was required to observe the decrease. In conclusion, these data suggest that a down regulator of an ob gene, e.g. a PPAR γ agonist such as a thiazolidinedione compound, is capable

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of increasing food intake and body weight, and thus treating cachexia, anorexia and other wasting diseases.

IV. Pharmaceutical Formulations and Modes of Administration

5 The particular compound that affects the disorders or conditions of interest can be administered to a patient either by themselves, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s). In
10 treating a patient exhibiting a disorder of interest, a therapeutically effective amount of a agent or agents such as these is administered. A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a
15 patient.

 The compounds also can be prepared as pharmaceutically acceptable salts. Examples of pharmaceutically acceptable salts include acid addition salts such as those containing hydrochloride, sulfate, phosphate,
20 sulfamate, acetate, citrate, lactate, tartrate, methanesulfonate, ethanesulfonate, benzenesulfonate, p-toluenesulfonate, cyclohexylsulfamate and quinate. (See e.g., PCT/US92/03736). Such salts can be derived using acids such as hydrochloric acid, sulfuric acid, phosphoric acid, sulfamic
25 acid, acetic acid, citric acid, lactic acid, tartaric acid, malonic acid, methanesulfonic acid, ethanesulfonic acid, benzenesulfonic acid, p-toluenesulfonic acid, cyclohexylsulfamic acid, and quinic acid.

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Pharmaceutically acceptable salts can be prepared by standard techniques. For example, the free base form of the compound is first dissolved in a suitable solvent such as an aqueous or aqueous-alcohol solution, containing the appropriate acid. The salt is then isolated by evaporating the solution. In another example, the salt is prepared by reacting the free base and acid in an organic solvent.

Carriers or excipients can be used to facilitate administration of the compound, for example, to increase the solubility of the compound. Examples of carriers and excipients include calcium carbonate, calcium phosphate, various sugars or types of starch, cellulose derivatives, gelatin, vegetable oils, polyethylene glycols and physiologically compatible solvents.

In addition, the molecules tested can be used to determine the structural features that enable them to act on the *ob* gene control region, and thus to select molecules useful in this invention. Those skilled in the art will know how to design drugs from lead molecules, using techniques such as those disclosed in PCT publication WO 94/18959, incorporated by reference herein.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.* for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture

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assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. For example, a dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal disruption of the protein complex, or a half-maximal inhibition of the cellular level and/or activity of a complex component). Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by HPLC.

The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., in The Pharmacological Basis of Therapeutics, 1975, Ch. 1 p. 1). It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the disorder of interest will vary with the severity of the condition to be treated and to the route of administration. The severity of the condition may, for

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example, be evaluated, in part, by standard prognostic evaluation methods. Further, the dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable
5 to that discussed above may be used in veterinary medicine.

Depending on the specific conditions being treated, such agents may be formulated and administered systemically or locally. Techniques for formulation and administration may be found in Remington's Pharmaceutical Sciences, 18th ed., Mack
10 Publishing Co., Easton, PA (1990). Suitable routes may include oral, rectal, transdermal, vaginal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous,
15 intraperitoneal, intranasal, or intraocular injections, just to name a few.

For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's
20 solution, or physiological saline buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

Use of pharmaceutically acceptable carriers to
25 formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular,
30 those formulated as solutions, may be administered

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parenterally, such as by intravenous injection. The compounds can be formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Agents intended to be administered intracellularly may be administered using techniques well known to those of ordinary skill in the art. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are efficiently delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, small organic molecules may be directly administered intracellularly.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active

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compounds into preparations which can be used pharmaceuti-
cally. The preparations formulated for oral administration
may be in the form of tablets, dragees, capsules, or
solutions. The pharmaceutical compositions of the present
5 invention may be manufactured in a manner that is itself
known, e.g., by means of conventional mixing, dissolving,
granulating, dragee-making, levitating, emulsifying,
encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral
10 administration include aqueous solutions of the active
compounds in water-soluble form. Additionally, suspensions of
the active compounds may be prepared as appropriate oily
injection suspensions. Suitable lipophilic solvents or
vehicles include fatty oils such as sesame oil, or synthetic
15 fatty acid esters, such as ethyl oleate or triglycerides, or
liposomes. Aqueous injection suspensions may contain
substances which increase the viscosity of the suspension,
such as sodium carboxymethyl cellulose, sorbitol, or dextran.
Optionally, the suspension may also contain suitable stabiliz-
20 ers or agents which increase the solubility of the compounds
to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be
obtained by combining the active compounds with solid
excipient, optionally grinding a resulting mixture, and
25 processing the mixture of granules, after adding suitable
auxiliaries, if desired, to obtain tablets or dragee cores.
Suitable excipients are, in particular, fillers such as
sugars, including lactose, sucrose, mannitol, or sorbitol;
cellulose preparations such as, for example, maize starch,
30 wheat starch, rice starch, potato starch, gelatin, gum

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tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

Some methods of delivery that may be used include:

- a. encapsulation in liposomes,
- b. transduction by retroviral vectors,

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- c. localization to nuclear compartment utilizing nuclear targeting site found on most nuclear proteins,
- d. transfection of cells ex vivo with subsequent reimplantation or administration of the transfected cells,
- e. a DNA transporter system.

5
10 All publications referenced are incorporated by reference herein, including the nucleic acid sequences and amino acid sequences listed in each publication. All the compounds disclosed and referred to in the publications mentioned above are incorporated by reference herein, including those compounds disclosed and referred to in articles cited by the publications mentioned above.

15 Other embodiments of this invention are disclosed in the following claims.

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TABLE 1. List of Candidate Compounds to Modulate ob

	CANDIDATE COMPOUNDS	REFERENCES
5	1) Compounds Modulating Glucocorticoids	*p.1213 ff, and references therein WO/92/16546, PCT/US92/02024 WO92/16658, PCT/US92/02014 US 4,981,787 US 5,071,773 R. Evans, <i>Science</i> 240:889-895 (1988)
10		
15	2) Thyroid hormones and thyromimetics	
20	3) Fibrates, free fatty acids & other agonists of PPAR such as Di (2-ethylhexyl)-phthalate & other plasticizers & herbicides such as 2, 4, 5 trichlorophenoxyacetic acid and leukotriene antagonists	#36 (see INDEX) S. Green, <i>Biochem. Pharm.</i> 43:393-400 (1992)
25	4) Antagonists of PPAR and subtype selective compounds (see Section II, item no. 43)	
30	5) RAR selective agonists & antagonists including subtype selective compounds	WO 91/07488 PCT/US90/06626
35	6) RXR selective agonists & antagonists including subtype selective compounds	PCT/US93/10094, WO94/15901, PCT/US92/11214, WO93/11755, PCT/US93/10166, PCT/US93/10204 WO94/15902 PCT/US93/03944 WO93/21146 Boehm, M.F. et al., <i>J. Med. Chem.</i> 37:2930-2941 (1994), #43
40		
45		

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	CANDIDATE COMPOUNDS	REFERENCES
	7) Estrogens-agonists & antagonists	*p. 1193 ff and references therein
5	8) Androgens-agonists & antagonists	*p. 1208 ff, and references therein US 4,144,270 US 3,847,988 US 3,995,060
10	9) Progestins-agonists & antagonists Non-steroid progestins	*p. 1200 ff, and references therein PCT/US93/03909 PCT/US93/10086 WO 94/24080
15	10) Mineralocorticoids-agonists & antagonists	*p. 1213 ff, and references therein
20	11) Insulin	from Obesity to Diabetes J.P. Felber, K.J. Acheson, Luc Tappy, John Wiley & Sons, 1993 pp. 33-44
25	12) Glucose, glucagon, free fatty acids, amino acids, sugars & other secretagogues such as buguanides (antidiabetics, e.g. AD4743, metformin & phenformin), pyroglyrides, linoglyrides & benzothenediones	#67, 68 compound (See INDEX)
30		
35	13) Non steroidal anti-inflammatory drugs	#61 (See INDEX)
	14) Prostacyclins	#61 (See INDEX)
40	15) Dihydroepiandrosterone and precursors and derivatives including Dioscorea spp. & aloe vera extracts & compounds derived therefrom	#15, 62, 64 (See INDEX)
45	16) Tumor necrosis factors	#51, 52, 53 (See INDEX)

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	CANDIDATE COMPOUNDS	REFERENCES
	17) Cytokines & related signaling molecules & growth factors	#54 (See INDEX)
5	18) Fetuin	#65 (See INDEX)
	19) Amylin agonists & antagonists	
	20) Prolactin	p. 452, Obesity
10	21) Niacin, acepimox & other nicotine acid derivatives	p. 765 in Obesity
	22) Triacscins	#66 (See INDEX)
15	23) Amphetamines & derivatives including fenfluramine & dexfenfluramine	pp. 414-418, in Obesity
	24) Endorphin antagonists	
20	25) Somatostatin	*p. 858 ff,
	26) Cholecystokinin	pp. 399-401 in Obesity
25	27) Bombesin	pp. 402-404 in Obesity (Brodoiff)
	28) Gastrin	p. 403 Obesity
30	29) Oral anti-diabetic agents & eventual antagonists	#67 (See INDEX)
	30) Corticotropin releasing hormone	#70 & 16 (See INDEX)
35	31) Adrenocorticotrophic hormones	pp. 545-547 in Obesity
	32) Melanocyte stimulating hormone	
40	33) Gastric inhibitory peptide	#71
	34) Growth hormone agonists & antagonists	pp. 103-104 in Obesity; Pathophysiology, psychology and treatment G.L. Blackburn, ed. Chapman & Hall (1994)
45		
50	35) Beta adrenergic agonists & antagonists including phenoxybenzamide fluloxetine	#56, 57 (See INDEX) pp. 766-769, 774 in Obesity,

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	CANDIDATE COMPOUNDS	REFERENCES
5		*Intracellular receptor general reference Comprehensive Medicinal Chemistry "The Rational Design, Mechanistic Study and Therapeutic Applications of Chemical Compounds," C. Hamsch, P.G. Sammes, John B. Taylor and John C. Emmett Vol. 3-Membrane and Receptors, Pergamon Press, Oxford, Ch. 16.3 Steroid Hormone Receptors pp. 1176-1226
10		*Obesity P. Bjorntorp and B.N. Brodoff, Eds. J.B. Lippencott Co., Philadelphia
15		

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CANDIDATE COMPOUNDS	REFERENCES
INDEX	
5	16. Muglia et al., <i>Nature</i> 373:427-432 (1995)
	36. Auwerx et al. <i>Hormone Research</i> 38:269-277 (1993)
10	43. Salazar-Olivo et al., <i>Biochem. Biophys. Res. Commun.</i> 204:257-263 (1994)
	51. Torti et al., <i>Science</i> 229:867-869 (1985)
	52. Kawakami et al., <i>J. Cell. Physiol.</i> 138:1-7 (1989)
15	53. Hotamisligil et al., <i>Science</i> 259:87-91 (1993)
	54. Gimble et al., <i>Mol. Cell. Biol.</i> 57:4587-4595 (1989)
20	56. Bouloumie et al., <i>J. Biol. Chem.</i> 269:30254-30259 (1994)
	57. Lowell et al., <i>Endocrinology</i> 126:1514-1520 (1990)
	59. Knight et al., <i>Mol. Endocrinol.</i> 1:36-43 (1987)
25	61. Negrel et al., <i>Biochem. J.</i> 257:399-405 (1989)
	62. Cleary et al., <i>Proc. Soc. Exp. Biol. Med.</i> 196 (1991)
30	64. Shantz et al., <i>Proc. Natl. Acad. Sci. USA</i> 86:3582-3856 (1989)
	65. Gaillard et al., <i>Biochim. Biophys. Acta</i> 846:185-191 (1985)
35	66. Tomoda et al., <i>J. Biol. Chem.</i> 266:4214-4219 (1991)
	67. Sparks et al., <i>J. Cell. Physiol.</i> 146:101-109 (1991)
40	68. Hiragun et al., <i>J. Cell. Physiol.</i> 134:124-130 (1988)
	70. Rohner-Jeanrenaud et al., <i>Endocrinology</i> 124:733-739 (1989)
45	71. Eckel, R. H. et al., <i>Diabetes</i> 28:1141-1142 (1979)

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Table 2. 5'-UTR sequences obtained by 5'-RACE with human
adipose total RNA.

Clone 1	CGGTTCGAAGGCCCAAGAAGCCCATCCTGGGAAGGAAAATG...
Clone 2	CGCAGGCCCAAGGTTGCAAGGCCCAAGAAGCCCATCCTGGGAAGGAAAATG...
Clone 3	AGGCCCAAGGTTGCAAGGCCCAAGAAGCCCATCCTGGGAAGGAAAATG...
Clone 4	AGGCCCAAGGTTGCAAGGCCCAAGAAGCCCATCCTGGGAAGGAAAATG...

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Table 3. 5'-UTR sequences obtained by 5'-RACE using human
adipose cDNA.

Clone 5	AGCGCCAACGGTTGCAAGGCCCAAGAAGCCATCCTGGGAAGGAAAATG...
Clone 6	AGCGCCAACGGTTGCAAGGCCCAAGAAGCCATCCTGGGAAGGAAAATG...
Clone 7	AGCGCCAACGGTTGCAAGGCCCAAGAAGCCATCCTGGGAAGGAAAATG...

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Table 4. Comparison of 5'-UTR sequence obtained from 5'-RACE
with the human genomic ob DNA sequence.

Clone 2	CGCAGCGCCACGGTTGCAAGGCCCAAGAAGCCCATCCTGGGAAGGAAAATG...
Genomic	...CTTGCAGTGTGTTCCTTCTGTGTCAGGCCCAAGAAGCCCATCCTGGGAAGGAAAATG...

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TABLE 5. Effects of administration of different doses of BRL 49653 on body mass, liver weight and weight of the epididymal fat pad.

		Body Mass	Epididymal fat	Liver
		(g)	(g)	(g)
5	Control	344 ± 22	2.5 ± 0.3	16.8 ± 1.3
	BRL 49653 (1mg/kg/day)	355 ± 21	3.3 ± 0.2*	17.9 ± 1.3
	BRL 49653 (2 mg/kg/day)	361 ± 18	3.8 ± 0.5*	18.9 ± 0.6
10	BRL 49653 (5 mg/kg/day)	338 ± 9	4.0 ± 0.6*	17.4 ± 1.8

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(*Statistically different from control, $p < 0.05$)

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Briggs et al.

10 (ii) TITLE OF INVENTION: Modulators of ob Gene and
Screening Methods Therefor

(iii) NUMBER OF SEQUENCES: 4

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

20

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1

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(vi) CURRENT APPLICATION DATA:

- 5 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- 10 (A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- 15 (A) NAME: Warburg, Richard J.
(B) REGISTRATION NUMBER: 32,327
(C) REFERENCE/DOCKET NUMBER: 211/128/6

20 (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (213) 489-1600
(B) TELEFAX: (213) 955-0440
25 (C) TELEX: 67-3510

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(A) Description: Sequence upstream of exon 1
including a promoter

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGCCATAGTC GCGCCGGAGC CTCTGGAGGG ACATCAAGGA TTTCTCGCTC CTACCAGCCA 60
CCCCCAAATT TTTGGGAGGT ACCCAAGGGT GCGCGCGTGG CTCCTGGCGC GCCGAGGCCC 120
TCCCTCGAGG CCCC GCGAGG TGCACACTGC GGGCCCAGGG CTAGCAGCCG CCCGGCACGT 180
CGCTACCCTG AGGGGCGGGG CGGGAGCTGG CGCTAGAAAT GCGCCGGGGC CTGCGGGGCA 240
GTTGCGCAAG TTGTGATCGG GCCGCTATAA GAGGGGCGGG CAGGCATGGA GCCC 294

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) Description: Sequence of exon 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGTAGGAATC GCAGCGCCAA CGGTTGCAAG

30

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10684 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) Description: Sequence between exon 1 and exon 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GTAAGGCCCC GCGCGCTCC TTCCTCCTTC TCTGCTGGTC TTTCTTGGCA GGCCACAGGG 60
CCCCACACAA CTCTGGATCC CGGGGAACT GAGTCAGGAG GGATGCAGGG CGGATGGCTT 120
20 AGTTCTGGAC TATGATAGCT TTGTACCGAG TTCTAGCCAG ATAGAAGGTT ACCGGGAGCT 180
GGGGAGCGTT GGATTGCTG CTGGGCTGTG CCGGTGCCCA GAAGGCAGGA CCTTGCAGAA 240
CCAGCCAGGT CCCTGGGAGA CTGTCAGACC CACCAACCTG GTGGCATTCT CAGAGCTGAG 300
ATGCATTGGA AATTGCCTTG GGCACATCCC CAAAGATCAG GATGTCCCAC CCCAGTCTGA 360
AGGAGATAAA GTTGGGGTA GGAGAGACGC AGATGCAAGT GATCAGTCTC AGTCCCAGAC 420
25 ATTGCCTTGC TCTGCGGGTA GGAATTCAGG ATTCATTTTC CAGGGAAGTT CCTGACCTCT 480
GAATGAGAGG GGCTGTGTAA GGCCAATGCC TGGGAGGAAG GCAAGGATGA GTAGAGGTGG 540
GGGGAAACAA GTGTCAGGAA GACTCAAAT CTCCAGAGA AATTGTGCAG GGTCTTACCA 600
GATCTGTCCT CAAAGCCATG CAAATTGCCT TCTTTGCAAT GCATACAATG AGGTGTCTCT 660
GGGGTCAGA ACTGTTATT AGGGAACCTC TAGCCAGGAC TGCTAAATAC GCGCTGTTGG 720
30 CCCACCAGGC TCACCTATAG CCTTCCTTCA GTCTGGGCTT GGTGTTGATT TCACTGTGGG 780
TGCCATCGCC TTTACACTCC TGTTCTATA GTTTAAAGAT AGTGGTGCTT TGGGAAAGTG 840
ACTCCTTAAA TACAGTTAGG TCCAAGTGAG ACAAGTGGCC TGGCTGTCAT TTCAGAATAG 900
CAGCTTCCAA GAGGTGATTA ATTTCTGTTG GAAGGGTGAT CTTTGGGGAG GTGGGTGAAG 960
AGCAGAGACT TGGTGGTACC GTCCAGGAG CACAGGCTCT CTTCTTTGC AGTGCAGAAT 1020

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GACCTCTGGC AGCCCGAGTT GTGTTTGTTT TGTAGGATTC TGAGGTGGGC CATGGGCAGC 1080
TGGAACTGGG GAATTTTGCC AATCTCTTTC ATATTAGGAT TGTCTGCAGA ACCAGATATG 1140
GAGGCTTCTA GCAACGTGAG TGCTCCTGTT CTAATGCCCT TAGAAACAAG AAGGCCACAC 1200
TGATCATTTT TCTCACTTAG GCAGGGAGAC AAGGCAAGAG AGAAACAGTG GATGCTTTTA 1260
5 GGTTCCTTTC CTCCCAAGC AGTTGTGGAC ATTGGGCTGA GGGGAACATT TCCACATTGG 1320
CTAAAGGAGC GTCCTCCTCA TATTTTGATC ATTTTATACC CAAAATAACT CTCTCTGGTA 1380
TTTGGGGAAA TATTTTCCTC CCGTCCATT CCAGGAAATG GCTCCAAGTG CCAAGGACAG 1440
AGCCAGGGAA GTTGCAATGA ATTCCTGCCC GTCAGCCCCA GGCAGATGCC TTGCACGTCT 1500
GAGTGGCCCA TGCAGAGCGT GGAGGTGGCC GCCACGGAAC CTGGGTCAAT GTCCCACCCC 1560
10 CGCTTAGATG CCACCAGGGG CGTGGGAGCC AAGGAGAGAA GAGGGGCTCC AGGAAGGTAG 1620
AGTCTCTGTG TCTTGTGCAT CTGTGAACAG CACTGGTATG ATTTAAAGGA AAATTGAGCC 1680
AAATTTTCGG GCAGTCAGTT ACCCCATCCC CACCGGGGTA GGAGTCTGGC AGCCGCAGCT 1740
CCATTCTGGC CAGTCGGCAG AGAGCCTTGA AATTCTTCTT TGTCCACACA GTTGTCTCAG 1800
AGAAACAGAG AGGTTGTTTC TGCTTAAAAA CAACACACTT GGTGTCTGGG CCCACAGACT 1860
15 CCTTTGCACT TATTCACGT GTGACAGCCA ATGTGCCTCG TTGCTTAGCA GACAGCATGT 1920
TACCGTCTTT CTGCTCAGT TTGTTAGCTC TATGGAATGG AATCTATAAT CAATGCCCAT 1980
ACCAACATTT CACTAATATC ATAGGAGATT TAGTCTCCAT CTGGGTGTAC ATTACATTTG 2040
CTCTGGGGTG CTCCAGGCTG GGGGGTTGCC AAGGAAGAGA AGAGAAACCG CAGAGAAGAC 2100
GGGAGGGCAG GGCAGGGGTC TCTGAGAAGG GGAGGGGTCC CAGAGTGCAG GAGCAGGAGC 2160
20 CAGGCTCATG AAAGGGGCCA CGGGCGGGAG TATCCAGGGA CGGCAGTCAA GATGGAGCAC 2220
AGCTTAGGAA GCTGAAGGGA ATCCTGGCCC ACCTGGGTGC TAGAGGGCAC ATAGGAAGTG 2280
CAGGAAGCAG ACCAAGGTCC CCAAGAGAGG GAGACCTGGA CGCTGAAGCA TTTTCAGTCT 2340
TTATTAAGAC AACTCCGTAA GAATTCCTGC TGGGCCAAAG TGAATTCTAG GATGCGACTT 2400
TAAGATGGGA GCAAGCGAAC CATTGAGGAG GCAGGTTACC CTAGTTAGCC AATGCAGATC 2460
25 GAGAATGGGA AATCTTTCAT TTATTCATGC AACAGATATT TATCGAAGCC CTGCCGTGTT 2520
CCAGGCCTGT GATAGATGCT GGAACAGGTA CAGAGATACA GGTGTCAATTA ATTGATCAGG 2580
GCAACCTCTC CTCTGAGTC TTGCTGGAGC TTCAGATGCC CCTCACACAG AGCTCGAGGG 2640
AGCCTCAACA ATTGATCAGA AGTCAGGCAC CATGGCTCAC GCATATAATC CCAGCACTTT 2700
GGGAGGCCAA GGCAGGTGGA TCACTGGAGC CCAGGAGTTC CAGATCAGCT GGGGCAACAT 2760
30 GGCAAAACCC CATCTCTATT AAAAAAAAAA AAAATTAATC GGATGTGATG GTACACACCT 2820
GTAGTCCCAG CTACTTGGGA GGCTGAGAGG TGGGAGAATT GCTTGAGCCC GGGAAAGTCGG 2880
GGGTCCAGTG AGCCTTGATC ACACCACTGC ACTCCAGCCT GAGTGACAGA GCAAGACCTT 2940
GACACACACA CACACACACA CACACACACA CAGATTAGAG CTGAAACAGG AGTAGAAACC 3000
TATCTGTATC TCTGATGAGA TCAGATTTTT CTGATGAACA GAAAGAATGT AACCCTGTGA 3060

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CTCACACCCT CTCTGCTGGT TACATATGTT AACACGATT CTCAAATGAG GCTTTTGGGT 3120
TGCAAATAAG AGAAAATCAC TCACGCTGGC CCTGTGTTTT TCAAATGTT TATGTGATC 3180
AACATTTGAA AAAAGAGCCG AGACTCTCAA GAGTGCATTA CCCACGGTAA GGGTGAATTT 3240
TACTTCTTGA CACTTATTTT TCTTACATGT ATCTATCTGT CTCAAATGAA AAATATATTT 3300
5 AGAAAGTTGA AAGCTATCCA AGTGAGTATA AGAAAAGAGT ATCTCACCCCT GAAGGCTAAG 3360
GACAGGGGAGG GCCACCAGGC CTCACGAGGA CCCAGGAACC ACAAAGAAGG CTAGGAAGGA 3420
GCACAGGCGG TGACCATACT CTGGCTCAGT GGCATATGTG GCTCTGGTCT CTCTCAGCTG 3480
TTCCATGTCAT ATGAGGCCAA ATGTGGCTAC CCTAGAGCTT CTGAGCCCTC AACAGAGATG 3540
AACTGGACTC TCTGCAGCCC CACTCTAAAT TCCTAAGAGA GAAATGATT GACCCAATCA 3600
10 GGGTCAGGAG AAGGAAGGGA GGAGGAAAGG GAGGAGAGAA GAGCCTCTTC GTCTCTTGCC 3660
TACCACTGGC CAGGCAATTG TAGCCAAGGG GGCTGGAGTG TAAATGCAA CATAGCCATC 3720
AAGGGTTGTG TATGTGTGTG TGTGTGCTG TGTGTGTGTA TGTGTGCTC TTGGGTAGGT 3780
TAGATCTCCC AGGAGGTCCC TACTAAACAG ACTTAAGCCC GCAAAATTTT AGCTCTCCAG 3840
CCTCACACAC TCCACCCCTC TACCATATTG AATCTTCCA AACCAACTAT GGCTTTCCCT 3900
15 AACTCCGAG CTTGGCCTGG AATGCCCTGC TTCCCTCTT TCCCTGGGG AACGCCTGTC 3960
CTTCAGGCCT CAGTTCACAC ACTGCCCTCC TTGCAAAGCT CTCCTCCCAT CCCCAGGATC 4020
CCTCTTCCCC TTTGTTCTTT GGGTTCTATG CTTCTTCCCT CATAACTCCC ACCAGTTGT 4080
GTTAAAATGA GTTGTTCAGG GTCCTGTCTG TTCCACTAGA TTCTGAGCAA CTGGAGAAC 4140
GAAGATCCAA ACTTCGCTGC CTTTATTTCC TCCTTTGTTT TTTTCTCATC CCAAGTCCC 4200
20 TTCCAATTG GAGTTATGAA GAAAGGAAGG AAGGAAGGT GGGAGGGAAG AACAGGAGG 4260
GATCCACAG GAGAATGTGT ATAGGGAGAG GACTCAGACT AGCTAAAGCT TTTCCCTCAT 4320
AATTAATAGC AAATACCATG TTACCTGAAT TTAATTCACA GTAGCATACA AAAGACTCGC 4380
TTTGTCTCCC CCATTGATGT CATCAGAGGG CTGTGGGCAG GCCTAATCTT GGCTCAGGAG 4440
GCCCTCCAGC CTGGATCTAA AGAGCAGCAG ATGGGCCAGG CTCGGTGGCT CATGCCTGTA 4500
25 ATCCCAGCAT TTTGGGAGGC CGAGGCGGGT GGATCACGAG GTCAGGAGTT TGAGACCAGC 4560
CTGGCCAAGA TGGTGAAGCC TCGTCTCTAC TAAAAATACA AAAATTAGCC AGGTGCGGTG 4620
GTGGCGCCT GTATTTCCAG CTACCCGGGA GGCTGAGGAG GCTGAGGCAG GAGAATCGCT 4680
TGAACCCGGG AGGCGGAGGT TGCAGTGAGC CGAGGTCACG CCACTGCACT CTAGCCTGGG 4740
CAACAGAGCA AGACTCCGTC AAAAAAAAAA TAAAAAATA AAAAAATAA AAAAAATAAG 4800
30 AGGAGCACAC ATCTCTGCCC ATCCTAACTC CCACTTTGAC ATTGAGGTCC CCAGGATGGA 4860
GGGTCTGCCT CCATCTGCCT TGTCCCTGTC AATGGTGGGA AGGTGATGGA GCTCAAGTCT 4920
AGAGGCCACC AGCTTCTTAG GGAGGTAGGA GGTGGAGGT GGGGTGCGGC CCCTGCACAC 4980
AACTGCCAAG TGAGGATGGG GGTGGGTCC ACCTGAGGAT AAGTAACAGT GAGGCTGGTG 5040
CAGAGGACCC AGGTGGAGGT AGACAGCAGA ATTTGTGGTG GGGTGGATGG CACATTATAT 5100

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AAGCCTCTCT TGCTGCCCTG TTTACTGAGA TTGTTTCATT ATCTTTTTTG GCITTTGTTT 5160
TTAAGAGATG GGGTCTTGCT GTGTCACACA GGCTGGAGTG CACTGTGTGA TCATACCTCA 5220
CTGCAGCCTC GACATCCTGG GCTCAGGCAA ACCTCCCACC TTGGCCTCCC AAGTAGCTGG 5280
GACCACAAGC GTTTGCCACC AACTCAGCT ATTTTATTTT TTATTTTTTT TTTTTTAGAG 5340
5 ATGGGGTCTT GCTGTGTCGC CCAGGCTGGT CTTGAACTCC TGGGCTCAAG CGATCCTCCT 5400
GCCTTGGCCT CCCAAAGCCC TGGGATTATA GGCTGAGGCC ACCACACCCA GCCACATTTC 5460
ATCTGTGCAG CTCCAGGGGC TCCACATTCT ACTCTTCTCA TTTCTTCTCC AGGGTACCCA 5520
TGGCAAGGGA TGAGGGTAGA AGATGGGGCA GCCAGGCCTT GATTAAAGGA GAAGGAAGGC 5580
AGCCTGTGGA GAGGGCAGCC CAGGGAGTGC AGAGAGAAGT GGCCCATGAG GGAGACAGCA 5640
10 GAGTGCAGCC TGCCTCCCAA ATGAGCACAC AGCCCACTGT GAGCCACCA TCTTCTAGA 5700
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15 GGGTCTTACA TTGTCAGCCC TTTGTCTCTG AGCTCAGACT TCCAATTCCA AGCGGCAGCT 6000
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GCTGAAAACA TTTGCTCCTC AGGGTGACAG AGGGAAGCT TTGCCTCCCT TCCTGGTGCT 6180
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20 AGCCACCATC TCCTAAACCC ACCTGTGTTT TTCCACCTCT GCCAGGGCTG CCTCTCTCTC 6300
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AAATTAGCCA GGCTGGGTGG TGCATGCCCG TAATTCAGC TACTCAGGAG GATGAAGCAA 7200
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CCAGCCTAGG TAAAGAACAA GACTCCATCT CAAAAATAAA TAAATAAAAA TAAATGTTCT 7320
TCCTTGCAAT GAAGTTAAAT ATGTAAATTC TCAAACCAGT TGCTTAAGGG CACAGTTTGG 7380
5 GTTCTTTTACC TATATTTTTA ACAAATATTT TATGTAAGTA GTTGACAAAA TCAAATACTG 7440
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GAGACCCAAA AGAACAGTGC CTTTAAAAG GCAGAGGTTA TGTCTCTCAC ACACCCCG 7980
15 CACAAGTCCA AGACCAGCAT GGCATCTCAG CTCATCAAC CTCAGGAACC GAGCTCCTGC 8040
AGCTCCCTGC CCTGCAGTTG ATAAGGTGAG GTCTTTGTCC TCCTGGTTCA AGATGGTGCT 8100
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AAGAGATGAA GGCACACGAC AGGTTCTGA GAGCTGGCAC AGGACACTTC TGCTTATATT 8220
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25 TCAGCTCCAT GTTTCAAGG AACCACAATT TATTTCCAGC ATCCACTGAA GCATATTATC 8640
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AGCTTTATTC CAGAGCAGGG TATTTGTTTC CAAATGCCAT GTTCCAGCA GCTGCCCTTG 9120
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GTGGCTCGCA CTCCTGCTTT CTGGATCTGA ATCCTGACTC TGTCATGGAC CTGTTTGA CT 9240
TTGGGCAAGT TGACTCCTAT TCCTGAGCCC CATATTTTTC TCTTCTGTAA AATTCAGATT 9300
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5 TGTCTTCATC AAGACCCAGA CGAGGAAGAA CACGAAAAGC GGAGATTAAT TTTACTGCCA 9480
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GGTAGAGAGC ATCTGTGTGT CACCATTGCA TCCTCGGTGC TGAGCACTGC GTCTGACATA 10020
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AAATGCAGAG GATGGGTGAG TAGCATAATC GCTAATGATA GGGTAATGAT AGAGCACATT 10200
TCACAACACC TTAAAGCCCT TTCACGTGCA TCAGATAATT TGATCCTCAT AGAAGCCTAG 10260
AGATAGATAT ATTACAGGGA TGAAGGTGGA GTATTTTGTG GTTATGTGAT ATGTTTAAAA 10320
20 TTATGCAGTG AGTAAATGAC TGGGTTCAAA CCAGACCTTA AAAGTCTGTT ATCTTTCCCT 10380
CGAGCATGCA ATGAAGTCTA CATCATCCCT ACCATGTCCA TTTGATCACA CCCTGGCCTC 10440
ACAGCTCTGT GGTCTACAGG ATACCTCATG GTGGTTTTAT TGACCAGACA ATAATCCTCT 10500
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GGGATGGTAG CCAGAGCAGA AAGCAAAGCT GATTTTCATC CCCGTCTGGT AATGTGGTTG 10620
25 GTAATGTGAA GATGGGTGTA TTCTGAGATA CCGGCTCCTT GCAGTGTGTG TTCCTTCTGT 10680
GTCA 10684

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 2921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(A) Description: Sequence upstream of the
transcription initiation site

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGCTTCTTT AAGGATGGAG AGGCCCTAGT GGAATGGGGA GATTCTTCCG GGAGAAGCGA 60
TGGATGCACA GTTGGGCATC CCCACAGAGG GACTGGAAAG AAAAAAGGCC TGGAGGAATC 120
AATGTGCAAT GTATGTGTGT TCCCTGGTTC AAGGGCTGGG AACTTTCTCT AAAGGGCCAG 180
20 GTAGAAAACA TTTTAGGCTT TCTAAGCCAA GGCAAAATG AGGATATTAC ATGGGTACTT 240
ATACAACAAG AATAACAAT TTACACAATT TTTTGTGAC AGAATTCAAA ACTTTATAGA 300
CACAGAAATG CAAATTTCCT GTAATTTCC CGTGAGAACT ATTCTTCTTT TGTTTTGTTT 360
TGCGACAGGG TTGCGCTGAT CCTCCCGCCT CAGTCTCCCT AAGTGCTGAG ATGTTGCAGG 420
AAGTCAGGGA CCCCGAACAG AGAGATCGGC TGGAGCCGTG GCAGAGGAAC ATAAATTTTG 480
25 AAGATTTTCA TTTAATATGG AACTTATCA GTTCCCAAAT AATACTTTTA TAATTTTTTA 540
TGCCTGTCTT TGCTTTAATC TCTTAATCCT GTTATCTTCA TAAGCTAAGG ATGTACGTCA 600
CCTCAGGACC ACTGTGATAA TTGTGTTAAC TGTACAGATT GATTGCAAAA CATGTGTGTT 660
TGAACAATAT GAAATCAGTG CACCTTGAAA AAGAGCAGAA TAACAGCAAT TTTTAGGGAA 720
CAAGGGAAGA CAACTATAAG GTCTGACTGC CTGCGGGGTC GGGCAAAGGG AGCCATATTT 780
30 TTCTTCTTGC AGAGAGCCTA TAAATAGACC TGCAAGTAGG AGAGATATTG CTAATTTCTT 840
TTGCTAGCAT GGAATATTAA TATTAACACC CTGGGAAAGG AATGCATTCC TGGGGGGAGG 900
TCTATAAATG GCCGCTCTGG GAATGTCTAT CCTACGCAAC GGAAGATAAGG ACTGAGATAC 960
GCCCTGGTCT CTGTCAGTAC CCTCAGGCTT ACTAGGGTGG TGAAAAACTC CGCCCTGGTA 1020
AATTTGTGGT CAGACCAGTT TTCTGCTCTC GAACACTGTT TTCTGTTGTT TAAGATGTTT 1080

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ATCAAGACAA TACGTGCACC GCTGAACACA GACCCCTTATC AGTAGTTCTC CTTTTTGCCC 1140
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5 CTGACACTTA TGGAAAATAG AAAGAACCTA CGTTGAAATA TTGGGGGCAG GTTCCCCCAA 1380
TATCTGGTGC CCAACGTGGG ATACTGAGAT TACAAGCATG AGCCACTGCA TCTGGCCTCT 1440
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20 GATGGAGACC CACAGTATGT CCAGAGTGTG CCCAAAGGCC ACAGTGCCCG CCTGGAGCCC 2280
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CTCGATTCTC CGCGTGCCAG AGAAGGGGTG GGACTTCAGA ACCCCCAACC CCGCAATCTG 2400
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25 GGGCGCAGCC GTATGCCCCA GCGCGCTCCG CCGAGCCCTT CACAGCCACC CCGCCCCGA 2580
CCGCGCCCCG CGCGGCTCGA AGCACCTTCC CAAGGGGCTG GTCCTTGCGC CATAGTCGCG 2640
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30 GCGGGGCGG GAGCTGGCG TAGAAATGCG CCGGGGCTG CCGGGCAGTT GCGCAAGTTG 2880
TGATCGGGCC GCTATAAGAG GGGCGGCAG GCATGGAGCC C 2921

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WHAT IS CLAIMED IS:

1. Isolated, purified, enriched or recombinant nucleic acid comprising a control region of a mammalian *ob* gene.
5
2. The nucleic acid of claim 1 comprising a control region of a human *ob* gene.
3. The nucleic acid of claim 2, wherein said
10 control region comprises the sequence 5' to exon 1 of said human *ob* gene cloned in a P1 plasmid or a portion thereof, wherein said P1 plasmid is selected from the group consisting of P1 clone 5135, P1 clone 5136, and P1 clone 5137, all of which are deposited at ATCC with accession numbers 69761,
15 69762, and 69763, respectively.
4. The nucleic acid of claim 2, wherein said control region comprises a promoter capable of initiating the transcription of said human *ob* gene.
20
5. The nucleic acid of claim 4, wherein said promoter comprises nucleotide -217 to -1 of said human *ob* gene or its complementary strand.
- 25 6. The nucleic acid of claim 4, wherein said promoter comprises nucleotide -2921 to -1 of said human *ob* gene or its complementary strand.

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19. The recombinant nucleic acid of claim 18,
wherein said control region and reporter sequence are inserted
in a vector.

5 20. The recombinant nucleic acid of claim 18,
wherein said mammalian ob gene is a human ob gene.

 21. The recombinant nucleic acid of claim 20,
wherein said control region comprises a promoter of said human
10 ob gene.

 22. The recombinant nucleic acid of claim 21,
wherein said promoter comprises nucleotide -2921 to
-1 of said human ob gene or its complementary strand.
15

 23. The recombinant nucleic acid of claim 22,
wherein said promoter comprises nucleotide -217 to
-1 of said human ob gene or its complementary strand.

20 24. The recombinant nucleic acid of claim 21
selected from the group consisting of pGL3B-OB1, pGL3B-OB2,
pGL3B-OB3 and pGL3B-OB4.

 25. The recombinant nucleic acid of claim 20,
25 wherein said control region comprises a positive transcription
element or a negative transcription element of said human ob
gene.

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26. The recombinant nucleic acid of claim 25, wherein said negative transcription element comprises comprises nucleotide -978 to -217 of said human ob gene or its complementary strand.

5

27. The recombinant nucleic acid of claim 25, wherein said negative transcription element comprises comprises nucleotide -1869 to -217 of said human ob gene or its complementary strand.

10

28. The recombinant nucleic acid of claim 25 selected from the group consisting of pGL3-OBA12 and pGL3-OBA5.

15

29. Method for screening for an agent modulating the expression of a mammalian ob gene, comprising the steps of:

providing a system comprising a control region of said mammalian ob gene and a reporter sequence transcriptionally linked to said control region wherein said control region is effective to initiate, terminate or regulate the transcription of said reporter sequence;

20

contacting a potential agent with said system; and comparing the level of transcription of said

25

reporter sequence with the level in the absence of said agent; wherein a measureable difference in the level of transcription of said reporter sequence is an indication that said agent is useful for modulating the expression of said mammalian ob gene.

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30. The method of claim 29, wherein said mammalian *ob* gene is a human *ob* gene.

31. The method of claim 29, wherein said control region and reporter sequence are inserted in a vector.

32. The method of claim 29, wherein said system further comprises a transcriptional protein.

33. The method of claim 32, wherein said transcriptional protein is expressed from a recombinant nucleic acid in said system.

34. The method of claim 32, wherein said transcriptional protein is an intracellular receptor.

35. The method of claim 34, wherein said intracellular receptor is PPAR γ or PPAR α .

36. The method of claim 32, wherein said transcriptional protein binds to a C/EBP site in SEQ. ID No.1.

37. The method of claim 29, wherein said control region and reporter sequence are inside a mammalian preadipocyte cell.

38. The method of claim 29, wherein said control region and reporter sequence are inside a mammalian adipocyte cell.

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39. The method of claim 29, wherein said control region and reporter sequence are inside a primary adipocyte cell.

5 40. The method of claim 29, wherein said control region and reporter sequence are inside a mammalian cell selected from the group consisting of COS, 3T3-L1, rat primary adipocyte, human primary adipocyte, mouse primary adipocyte and immortalized adipocyte cell.

10 41. The method of claim 29, wherein said agent is selected from the group consisting of glucocorticoids; thyroid hormones; thyromimetics; fibrates, free fatty acids and other agonists of PPAR including Di-(2-ethylhexyl)-phthalate,
15 plasticizers and herbicides including 2, 4, 5-trichlorophenoxyacetic acid and leukotriene antagonists; antagonists of PPAR and PPAR subtype selective compounds; RAR selective agonists and antagonists including subtype selective compounds; RXR selective agonists and antagonists including
20 subtype selective compounds; estrogens and other agonists and antagonists of ER; androgens and other agonists and antagonists of AR; progestins and other agonists and antagonists of PR; non-steroid progestins; mineralocorticoids and other agonists and antagonists of MR; insulin; glucose;
25 glucagon; free fatty acids; amino acids; sugars and other secretagogues including biguanides; antidiabetics including metformin and phenformin; pyroglyrides; linoglyrides and benzothenediones; non-steroidal anti-inflammatory drugs; prostacyclins; dihydroepiandrosterone and stimulators,
30 precursors and derivatives thereof including Dioscorea and

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aloe vera, and extracts and compounds derived therefrom; tumor
necrosis factors; cytokines and related signaling molecules;
growth factors; fetuin; Amylin agonists and antagonists;
prolactin; niacin; Acepimox and other nicotinic acid
5 derivatives; triacsins; amphetamines and derivatives including
fenfluramine and dexfenfluramine; endorphin antagonists;
somatostatin; cholecystokinin; bombesin; gastrin; oral anti-
diabetic agents; corticotropin releasing hormone;
thiazolidinedione compounds; adrenocorticotrophic hormones;
10 melanocyte stimulating hormone; gastric inhibitory peptide;
growth hormone agonists and antagonists; β -adrenergic agonists
and antagonists including phenoxybenzamide; fluloxetine;
neuropeptide Y and agents modulating neuropeptide Y activity
or expression.

15

42. The method of claim 29 used to screen for an
agent increasing the transcription of said mammalian ob gene,
wherein said potential agent is selected from the group
consisting of PPAR γ antagonist, C/EBP protein agonist, PPAR α
20 agonist, glucocorticoid, insulin derivative, insulin
secretagogue, insulin sensitizer and insulin mimetic..

43. The method of claim 29 used to screen for an
agent decreasing the transcription of said mammalian ob gene,
25 wherein said potential agent is selected from the group
consisting of PPAR γ agonist, C/EBP protein antagonist, PPAR α
antagonist, glucocorticoid antagonist, and insulin antagonist.

44. The method of claim 43, wherein said PPAR γ
30 agonist is a thiazolidinedione compound.

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45. Method for modulating the expression level of a mammalian *ob* gene, comprising the step of administering to a mammalian cell or a mammal a composition comprising an effective amount of a modulator of a control region of said mammalian *ob* gene.

46. The method of claim 45, wherein said modulator increases the expression level of said mammalian *ob* gene.

47. The method of claim 46, wherein said modulator is a glucocorticoid.

48. The method of claim 47, wherein said glucocorticoid is hydrocortisone, triamcinolone or dexamethasone hydrocortisone.

49. The method of claim 46, wherein said modulator is selected from the group consisting of insulin, insulin derivative, insulin secretagogue, insulin sensitizer and insulin mimetic.

50. The method of claim 46, wherein said modulator is a PPAR γ antagonist.

51. The method of claim 46, wherein said modulator is a PPAR α agonist.

52. The method of claim 46, wherein said modulator is a C/EBP protein agonist.

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53. The method of claim 45, wherein said modulator is a free fatty acid or fish oil.

54. The method of claim 45, wherein said modulator lowers the expression level of said mammalian *ob* gene.

55. The method of claim 54, wherein said modulator is a PPAR γ agonist.

56. The method of claim 55, wherein said PPAR γ agonist is a thiazolidinedione compound.

57. The method of claim 56, wherein said thiazolidinedione compound is BRL49653, pioglitazone or troglitazone.

58. The method of claim 54, wherein said modulator is selected from the group consisting of C/EBP protein antagonist, PPAR α antagonist, glucocorticoid antagonist, or insulin antagonist.

59. Method for treating a host having cachexia, anorexia or any wasting disease characterized by loss of appetite, insufficient food intake or body weight loss, comprising the step of administering to said host a composition containing a pharmaceutically effective amount of a down regulator of *ob* gene expression.

60. The method of claim 59 wherein said down regulator is a PPAR γ agonist.

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61. The method of claim 60 wherein said PPAR γ agonist is a thiazolidinedione compound.

62. The method of claim 61 wherein said
5 thiazolidinedione compound is BRL49653, pioglitazone or troglitazone.

63. The method of claim 59, wherein said modulator
is selected from the group consisting of C/EBP protein
10 antagonist, PPAR α antagonist, glucocorticoid antagonist, or insulin antagonist.

64. Method for changing the body weight or body fat
content of a host, comprising the step of administering to
15 said host a composition containing a pharmaceutically effective amount of an up regulator or down regulator of *ob* gene expression.

65. The method of claim 64, wherein said up
20 regulator is selected from the group consisting of glucocorticoid, hydrocortisone, triamcinolone and dexamethasone hydrocortisone, insulin, insulin derivative, insulin secretagogue, insulin sensitizer, insulin mimetic, PPAR γ antagonist, PPAR α agonist, and C/EBP protein agonist.

25

66. The method of claim 64, wherein said down
regulator is selected from the group consisting of PPAR γ agonist, thiazolidinedione, BRL49653, pioglitazone or troglitazone, free fatty acid, fish oil, C/EBP protein

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antagonist, PPAR α antagonist, glucocorticoid antagonist, and insulin antagonist.

5 67. Method for treating a host having a body weight more than about 20% in excess of the ideal body weight, comprising the step of administering to said host a composition containing a pharmaceutically effective amount of an up regulator of *ob* gene expression.

10 68. Method for treating a host having hyperlipidemia, hypercholesterolemia, type II adult onset diabetes, obesity related infertility, comprising the step of administering to said host a composition containing a pharmaceutically effective amount of an up regulator of *ob* gene expression.

15 69. Method for changing the body weight or body fat content of a mammalian animal comprising the step of administering to said animal a composition containing an effective amount of a modulator of *ob* gene expression.

20 70. A pharmaceutical composition comprising a pharmaceutically effective amount of a modulator of a mammalian *ob* gene control region.

25 71. The pharmaceutical composition of claim 70, wherein said mammalian *ob* gene is a human *ob* gene.

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72. The pharmaceutical composition of claim 71, comprising a label stating to the effect that the composition is approved by the FDA in the United States for treating a disease or pathological condition selected from the group consisting of obesity, diabetes, infertility, cardiovascular diseases, hypertension, hyperlipidemia, hypercholesterolemia, cachexia and anorexia.

73. The pharmaceutical composition of claim 70, wherein said modulator is a glucocorticoid.

74. The pharmaceutical composition of claim 73, wherein said glucocorticoid is hydrocortisone, triamcinolone, or dexamethasone.

75. The pharmaceutical composition of claim 70, wherein said modulator is selected from the group consisting of insulin, insulin derivative, insulin secretagogue, insulin sensitizer or insulin mimetic.

76. The pharmaceutical composition of claim 70, wherein said modulator is a PPAR γ agonist.

77. The pharmaceutical composition of claim 76, wherein said PPAR γ agonist is a thiazolidinedione compound.

78. The pharmaceutical composition of claim 77, wherein said a thiazolidinedione compound is BRL49653, troglitazone or pioglitazone.

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79. The pharmaceutical composition of claim 70,
wherein said modulator is selected from the group consisting
of C/EBP protein antagonist, PPAR α antagonist, glucocorticoid
antagonist, insulin antagonist, PPAR γ antagonist, PPAR α
5 agonist, C/EBP protein agonist, free fatty acid and fish oil.

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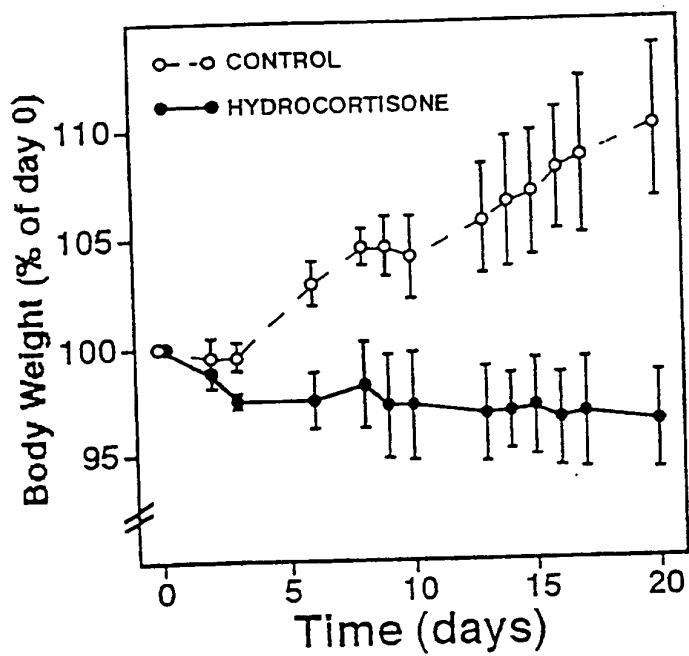


FIGURE 1

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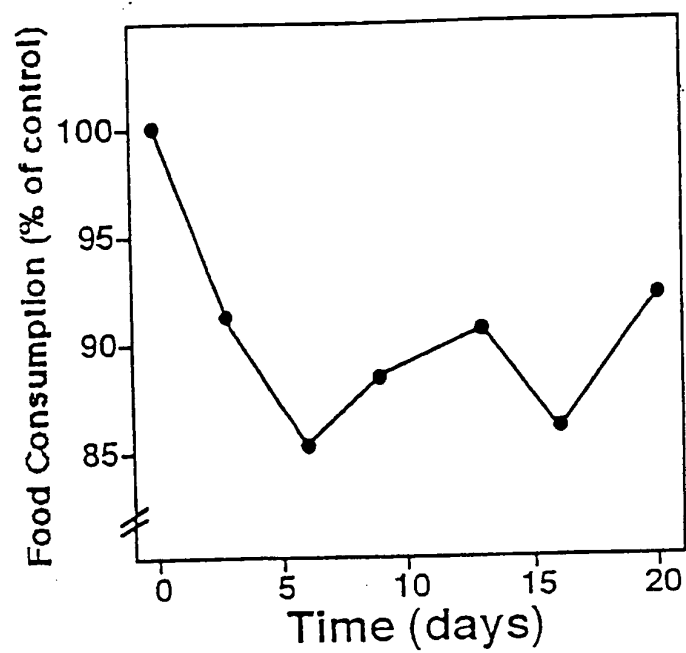


FIGURE 2

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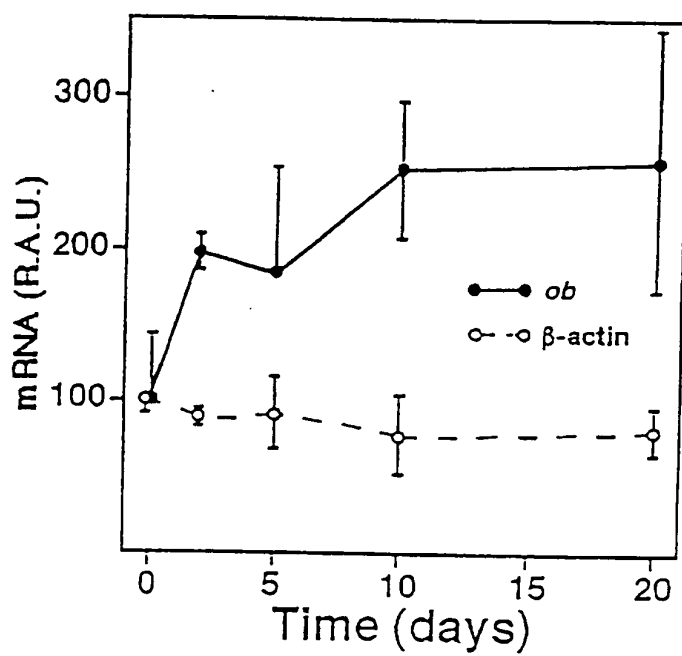


FIGURE 3

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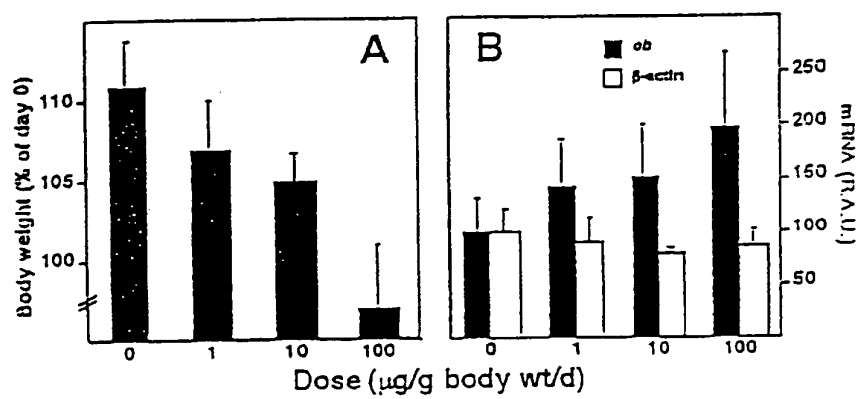


FIGURE 4

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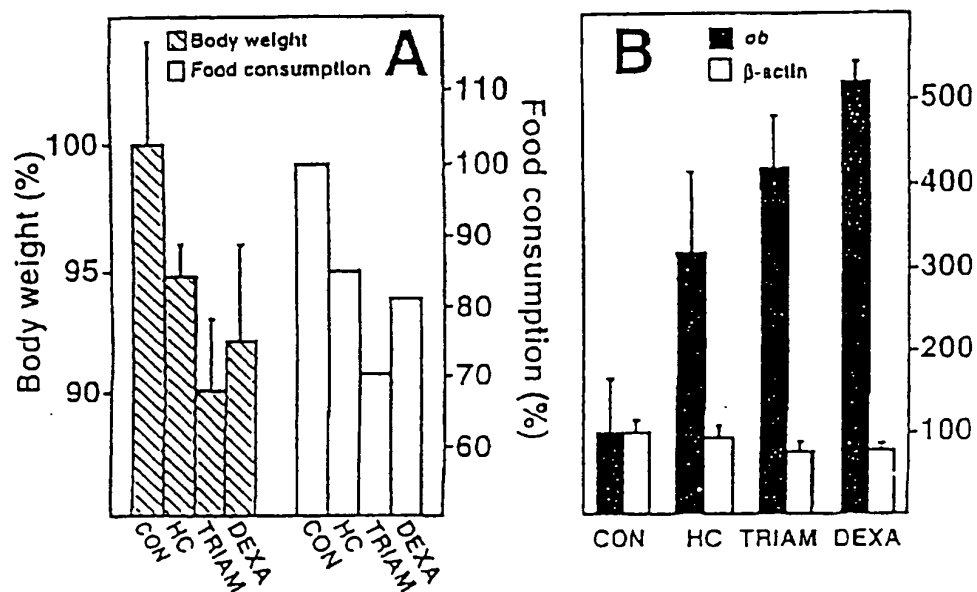


FIGURE 5

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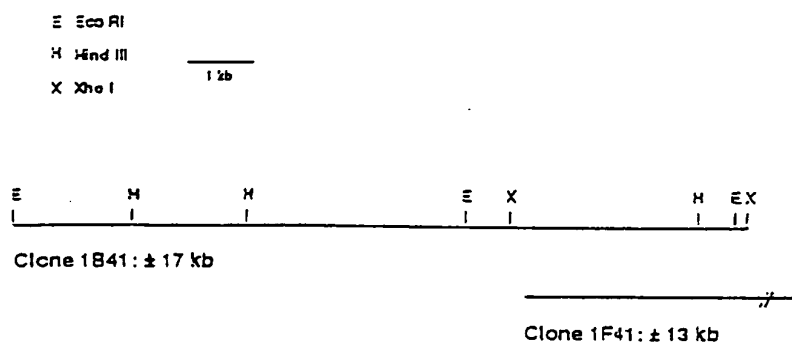


FIGURE 6

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Effect of food and insulin on in vivo
ob gene expression

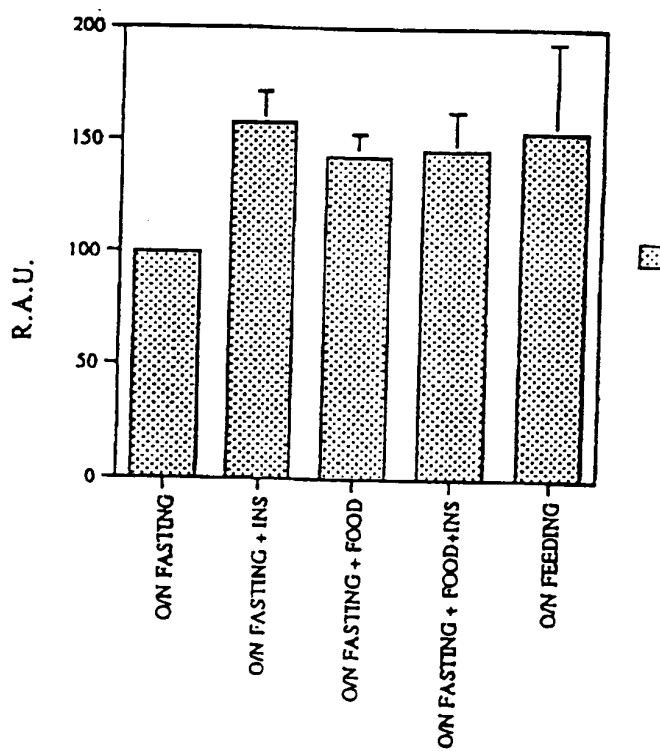


FIGURE 7

[illegible]

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$\bar{L} = \text{Ecoll}$
 $\bar{X} = \text{Xhol}$
 $\bar{H} = \text{HindIII}$

Clone 1B41
 ≈ 17000 bp

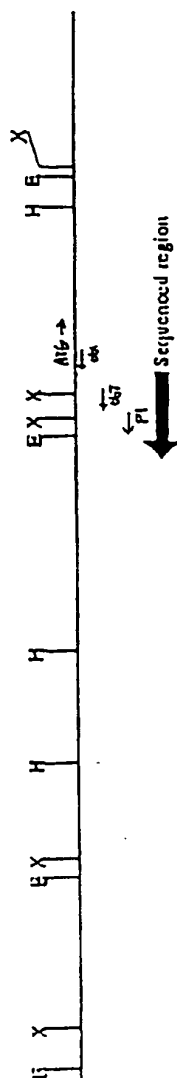


FIGURE 8

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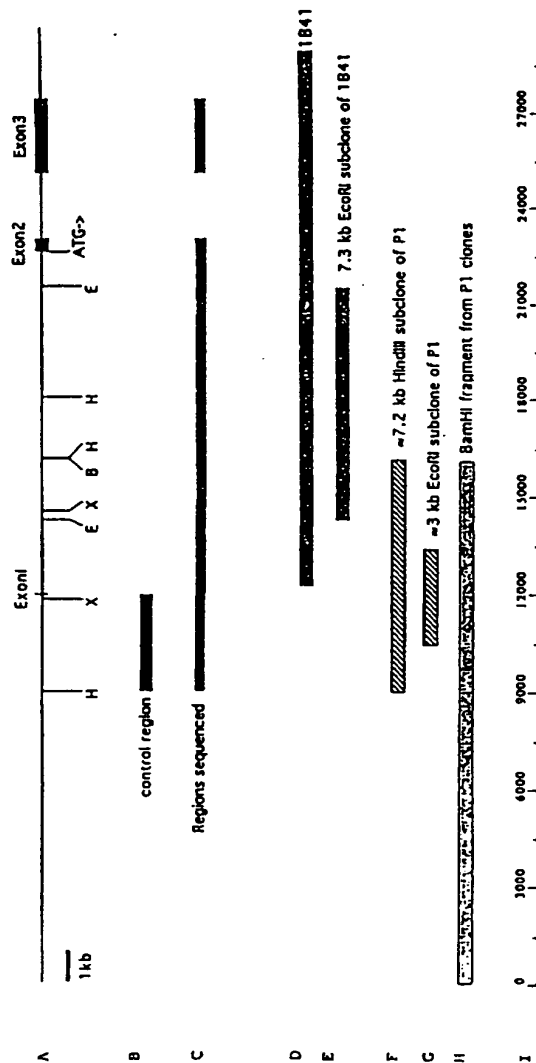


FIGURE 9

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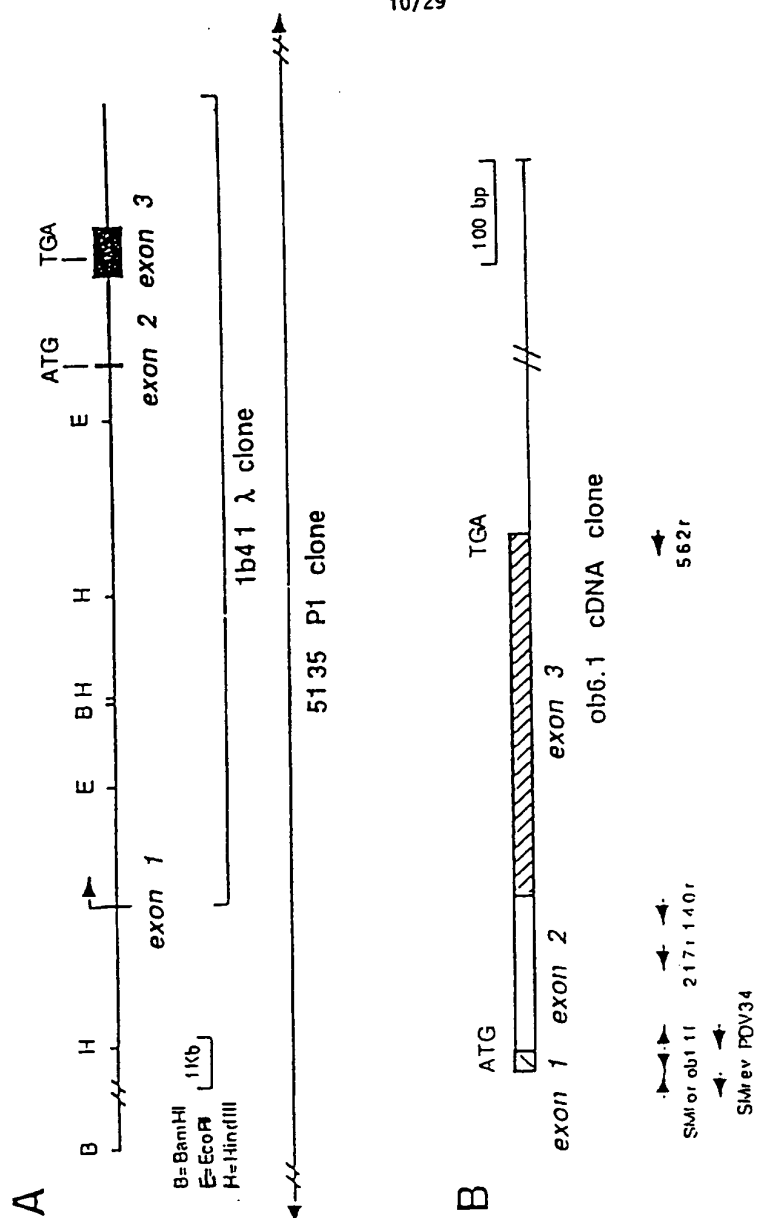


FIGURE 10

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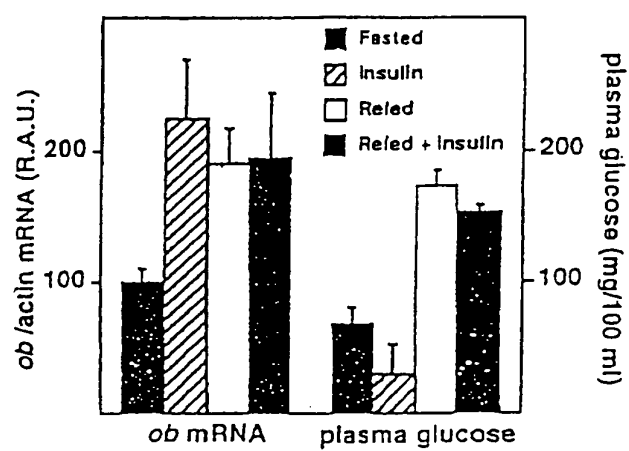


FIGURE 11

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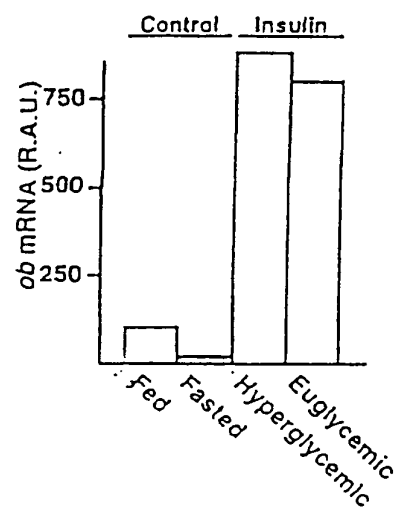


FIGURE 12

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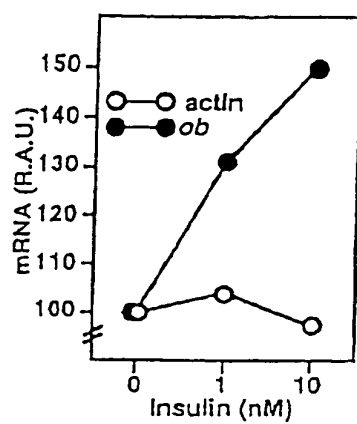


FIGURE 13

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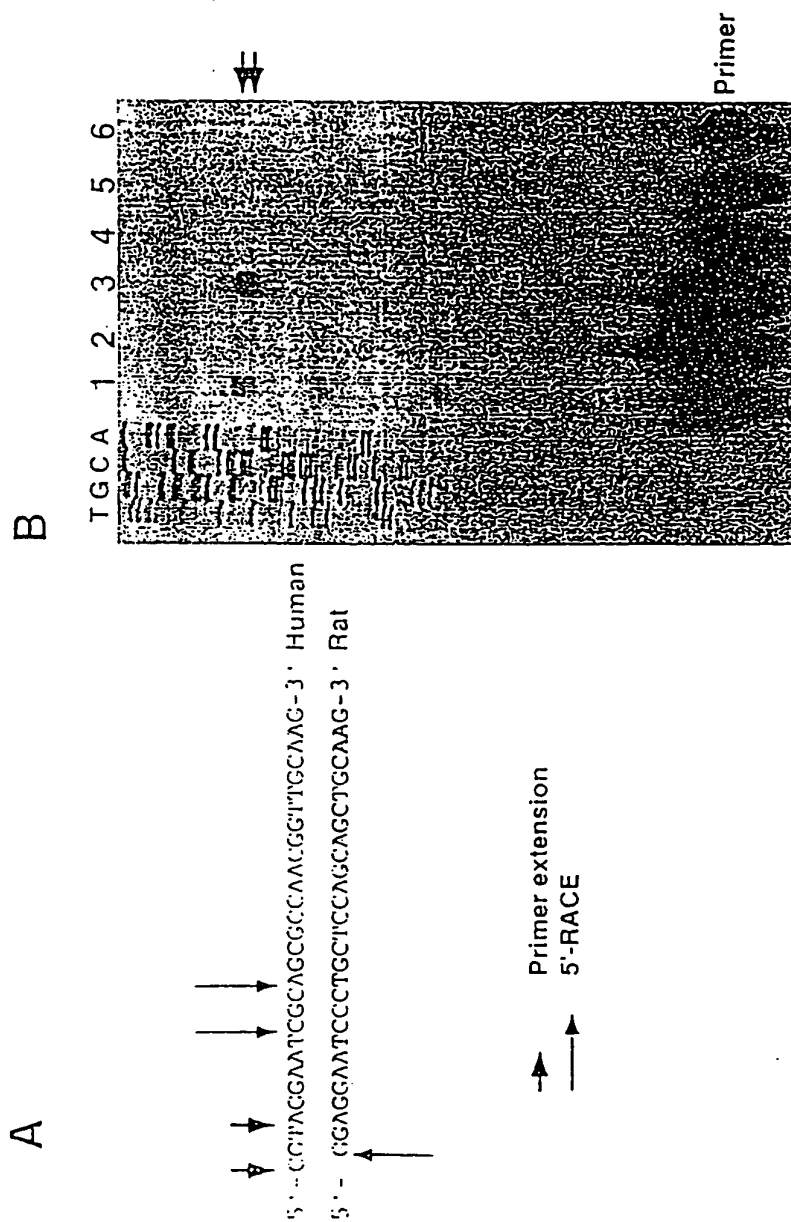


FIGURE 14

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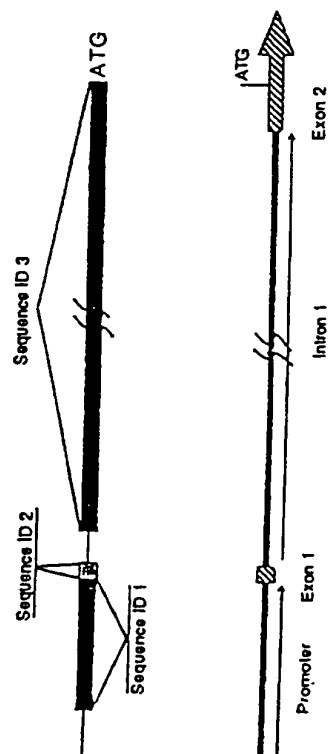


FIGURE 15

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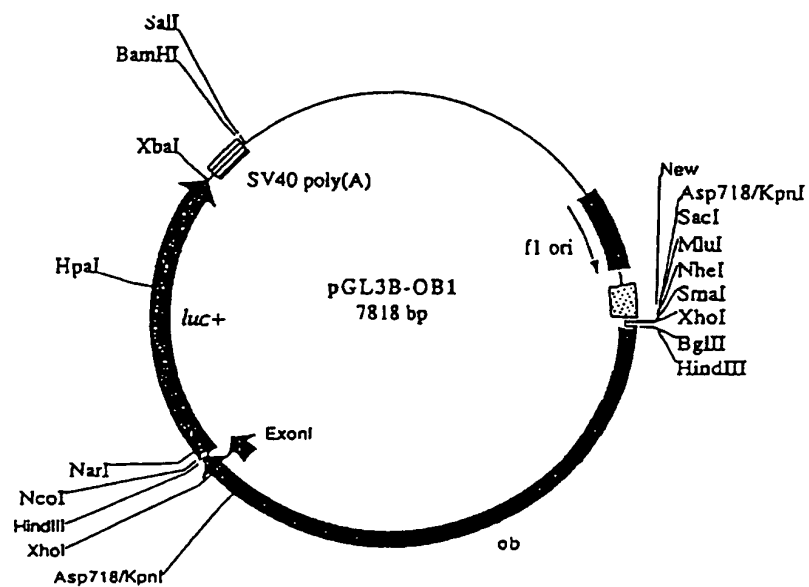


FIGURE 16 (a)

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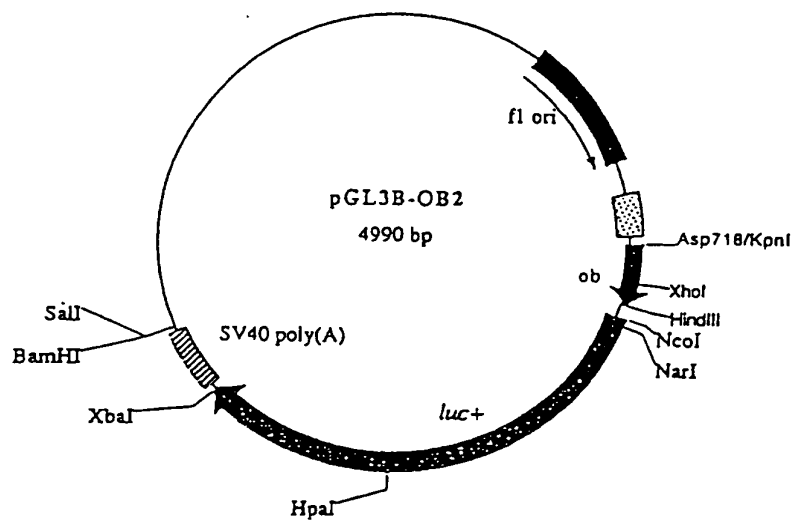


FIGURE 16 (b)

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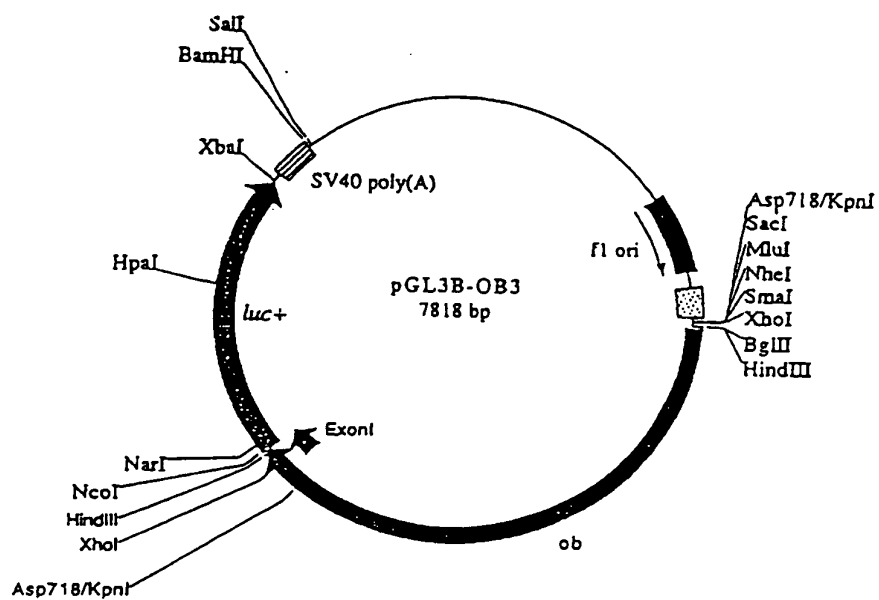


FIGURE 16 (c)

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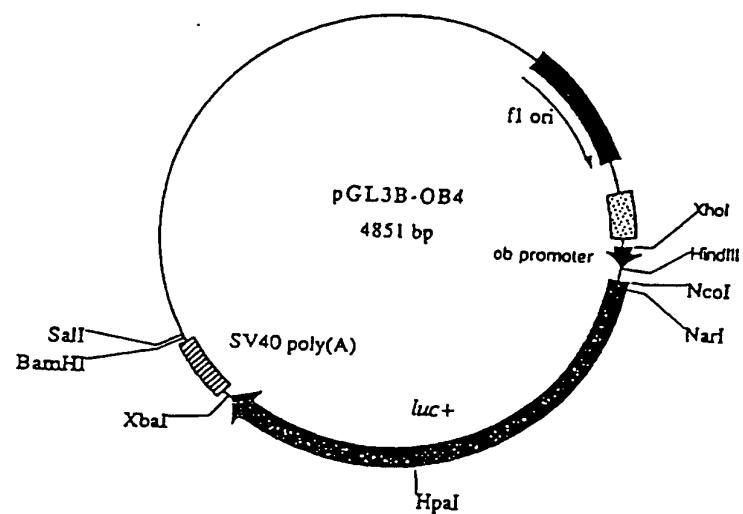


FIGURE 16 (d)

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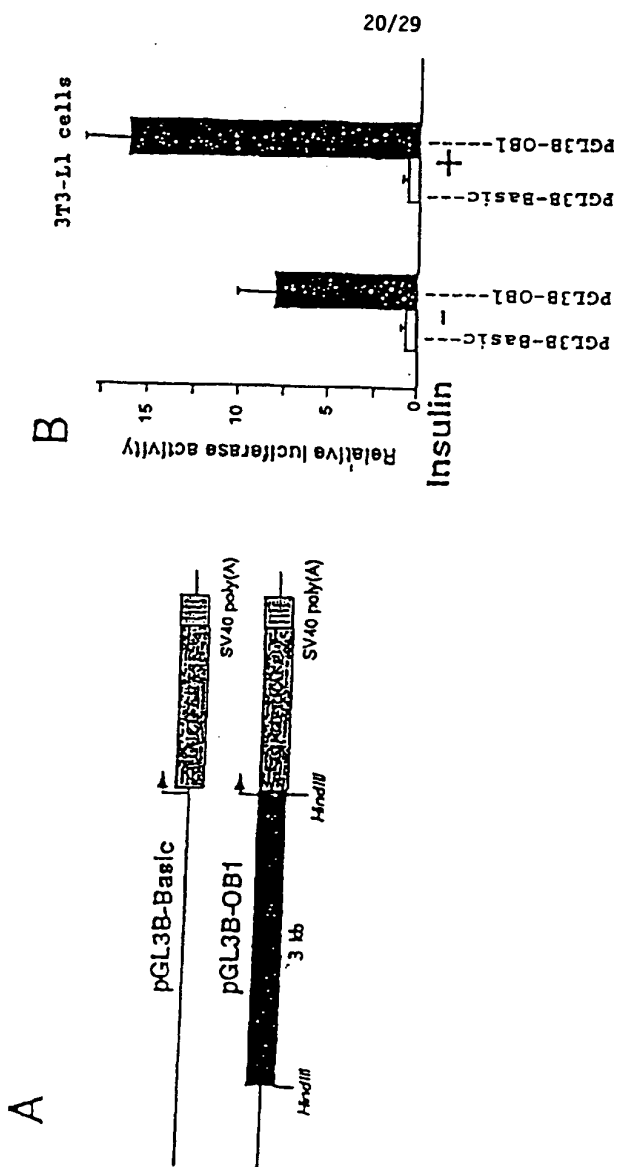


FIGURE 17

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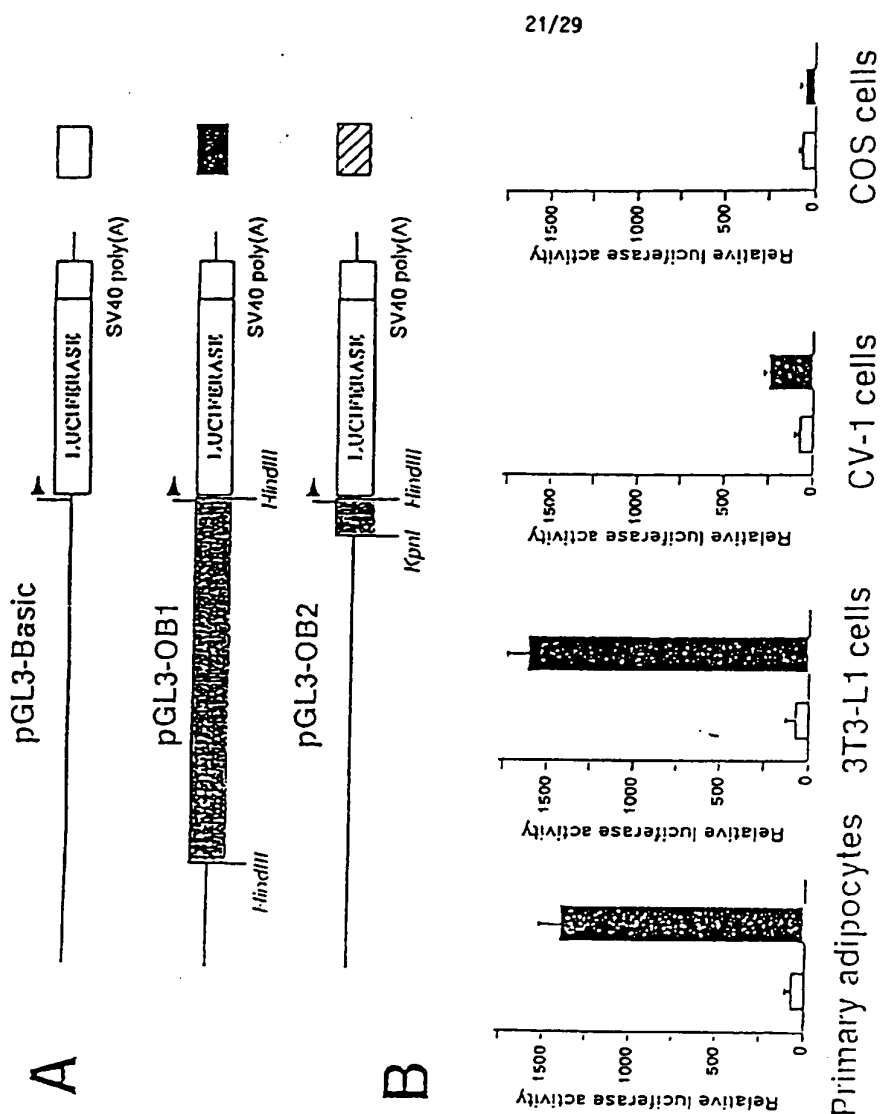


FIGURE 18

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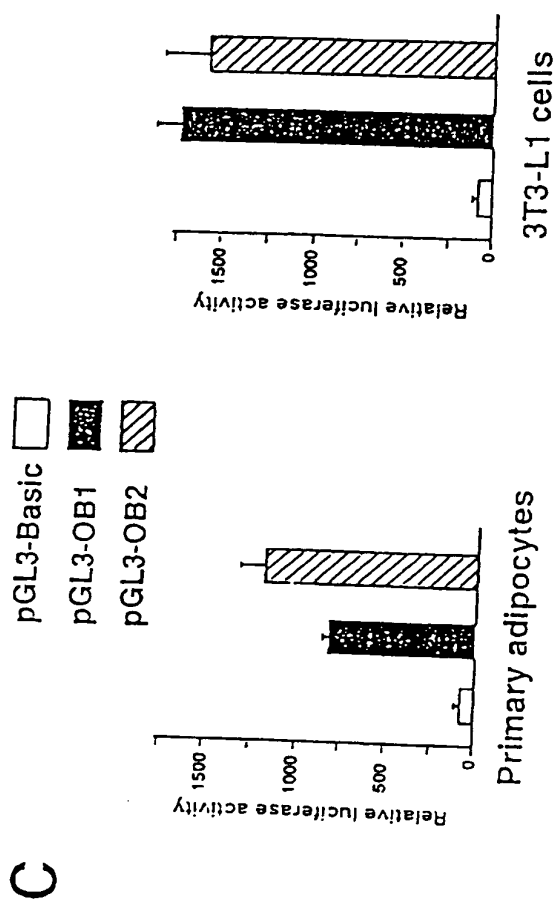


FIGURE 18

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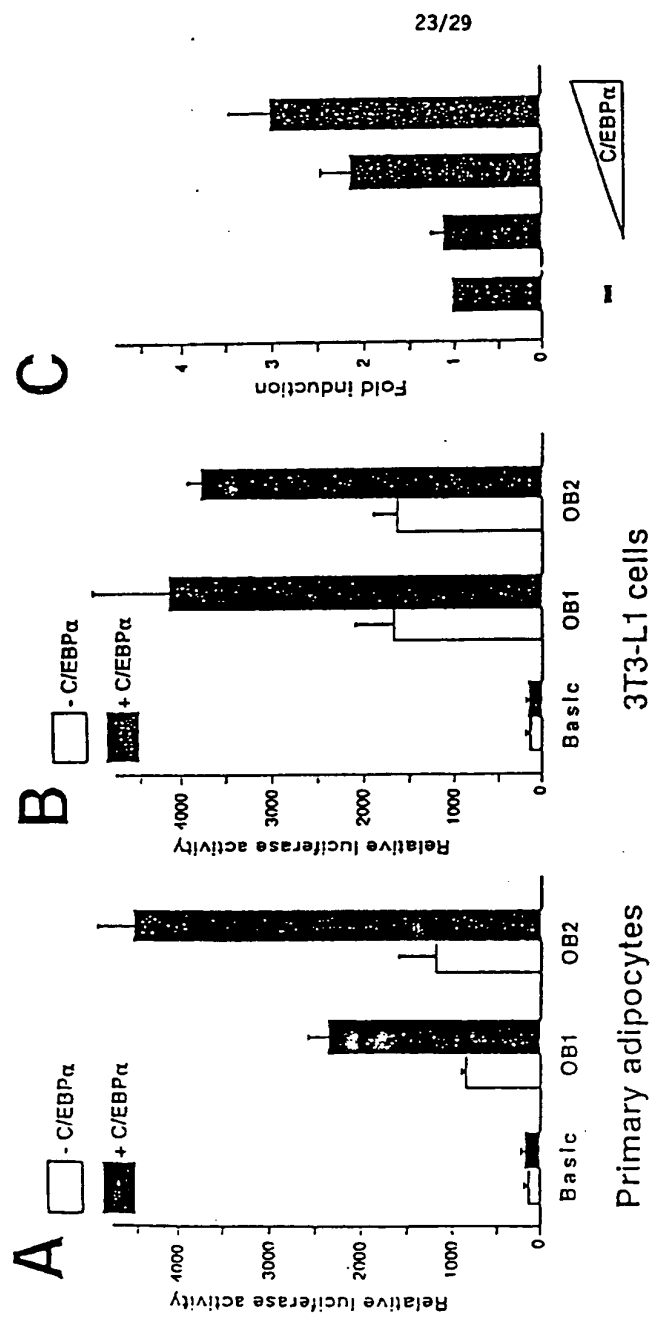


FIGURE 19

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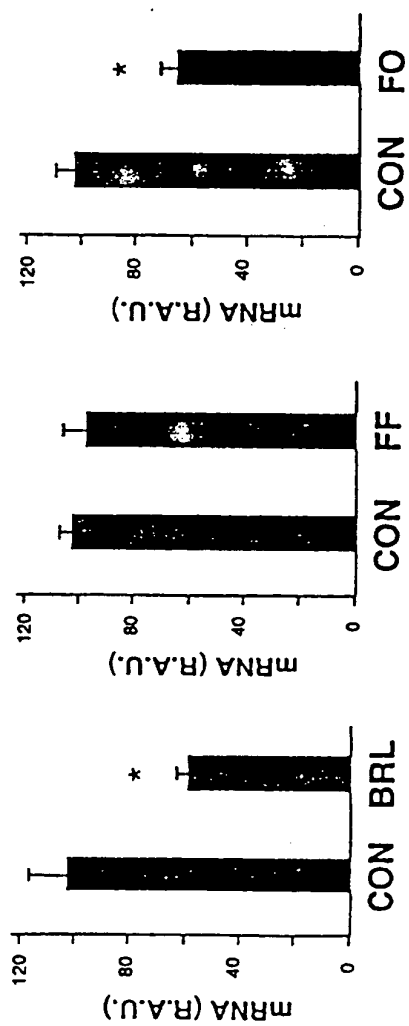


FIGURE 20

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FIGURE 21

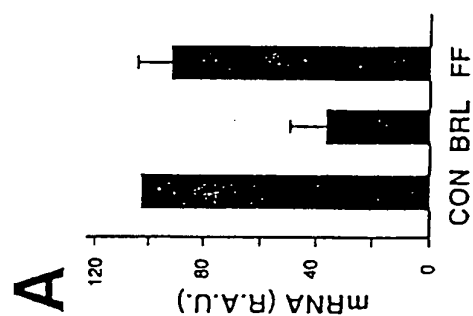


FIGURE 21A

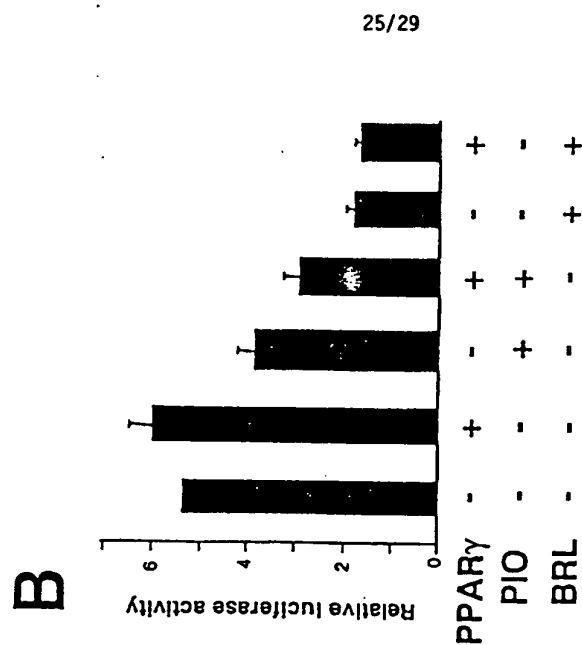


FIGURE 21B

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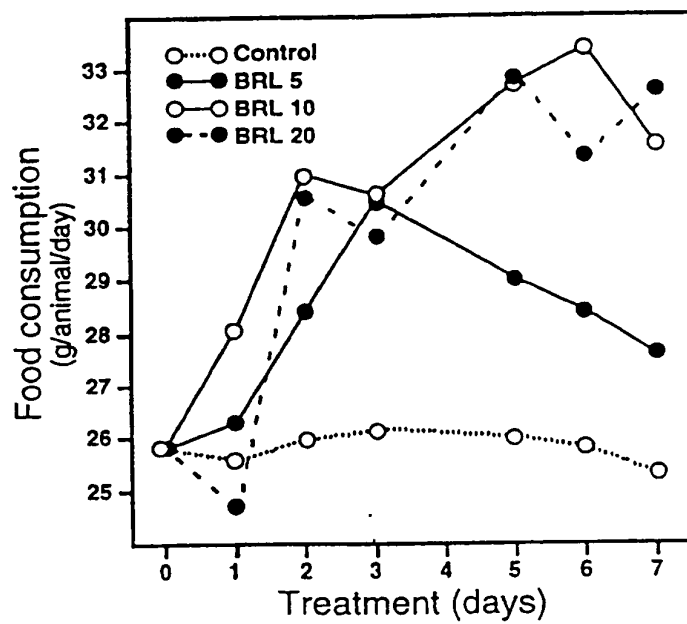


FIGURE 22

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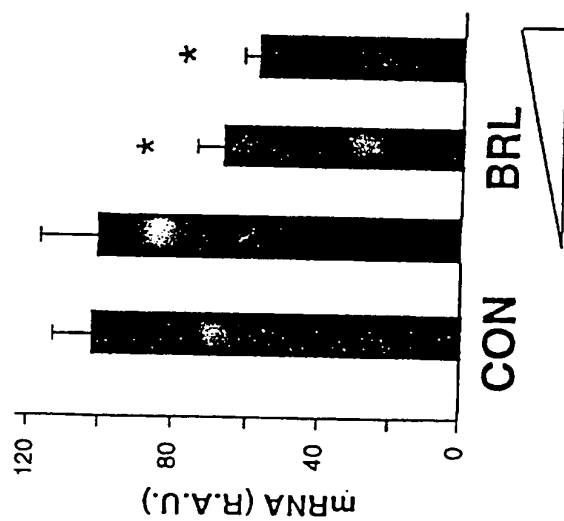


FIGURE 23

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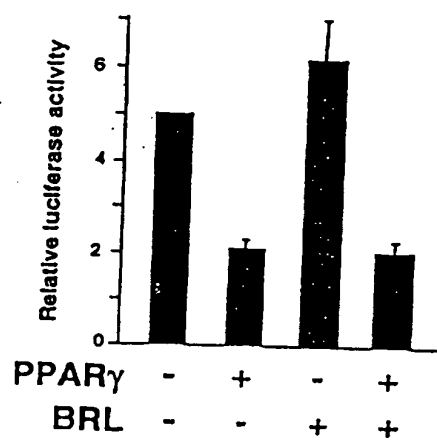


FIGURE 24

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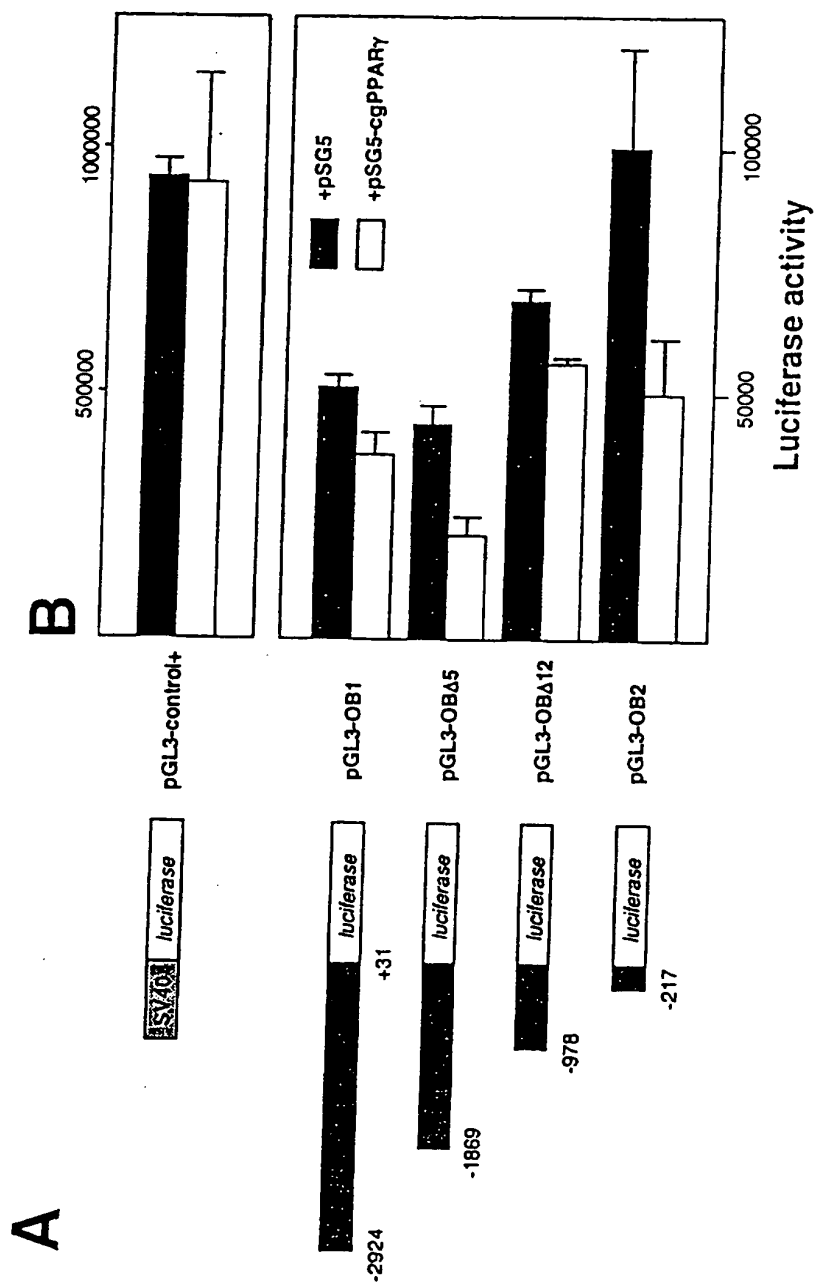


FIGURE 25